## STIC-Biotech/ChemLib

195090

From:

Dunston, Jennifer A.

Sent:

Monday, July 10, 2006 3:30 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence Search 10/659782

Please search nucleotides 112-462 of SEQ ID NO: 11 and the amino acid sequence of SEQ ID NO: 32 against the commercial and interference protein databases.

Thank you.

Jennifer Dunston, Ph.D. USPTO Art Unit 1636 REM 2B76 Mailbox: REM 2C70 (571) 272-2916

Type of Search
NA# AA#:
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:\_\_\_\_\_
DIALOG:\_\_\_
QUESTEL/ORBIT:\_\_\_\_
LEXIS/NEXIS:\_\_\_
SEQUENCE SYSTEM:\_\_\_
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Other (Specify):\_\_\_\_\_

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		49	

Scoring table:

Total number

Database

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Searched:

score:

Perfect

Title:

Run on:

Sequence:

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Human PRO
Human sec
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Human PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to alternative splice variants of the obesity and/or diabetes related genes and their corresponding proteins. The invention also relates to compositions, reagents, kits and methods for diagnosing, monitoring and treating obesity and/or diabetes. The composition and methods are useful for diagnosing, monitoring and
                 Abo25061
Abu58977
Abu53355
Aae33409
Abu57066
Abu607066
Abu10892
Abu10892
Abu10892
Abu10892
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Ada76392
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Ada19042
Ada19042
Ada16034
Ada86701
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/note= "Encoded by CATCTCTGG"
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                 ABO25061
ABU58977
ABU58977
ABU58973
ABU59420
ABU67066
ABU92186
ABU10892
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Misc-difference 64. .65
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 N-PSDB; ADY78053
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 ADY78074;
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IID ADY

IID ADY

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BDB HUM

BD HUM

BD
   Ady78074 Human ghr
Adx66754 Human ghr
Ade33410 Human sin
Ade37210 Frotein d
Ady87236 Human sig
Adb20101 Zsig33 pr
Adb62649 Human zsi
Adb60511 Human ghr
Abb78319 Amino aci
Ade15883 Human zsi
Ade15883 Human zsi
Ade15883 Human zsi
Adb60515 Human ghr
Abu58046 Human gec
Abo17836 Novel hum
Abu60555 Human gec
Abu13337 Human gec
Abu13337 Human RRO
Abu6790 Human RRO
Abu6790 Human RRO
Abu72522 Novel hum
Abu66790 Human RRO
Abu58011 Novel hum
Abu66790 Human RRO
Abu58011 Human RRO
Abu58011 Novel hum
Abu66790 Human RRO
Abu59211 Human RRO
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                                                                                                                                                                                                                        1 MPSPGTVCSLLLLGMLWLDL.......PPSSRERSRRSHQPSCSPEL 117
                                                                                                                       July 11, 2006, 16:56:38 ; Search time 196 Seconds
                   GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          2589679 seqs, 457216429 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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AAM38890
AAB60511
ABB78319
AAE23838
AAE15883
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AAE33410
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AAY87236
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geneseqp2001s:*
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Maximum DB seq length: 200000000
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treating obesity and/or diabetes. These may also be used in drug screening purposes and in gene therapy. The present sequence is the human ghrelin (GHRL) variant protein. This protein is encoded by an obesity and diabetes related gene.
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                                                                                                                                                                                                                                     QORHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCSPEL 117
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                                                                                                                                           Gaps
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                                                                                                             Length 116;
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                                                                                                          97.7%; Score 605.5; DB 9;
99.1%; Pred. No. 8.7e-61;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                ADK66754 standard; protein;
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                                                                                                       Query Match
Best Local Similarity 99.1
Matches 116; Conservative
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ANDERSON L L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                              Sequence 116 AA;
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(ANDE/)
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Length 60;

Score 198; DB 8; Pred. No. 1.2e-14;

31.9%; 88.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                      Ghrelin, preproghrelin, GHS-R 1b; benign prostatic hyperplasia; therapy; breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
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Pred. No. 2.1e-14;
0; Mismatches 5;
 Mismatches
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17-DEC-2001; 2001AU-00009567.
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 Conservative
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N-PSDB; AAD50726.
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les 39; Conserv
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 39;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated vith gastrointestinal cell contractility, secretion of digestive enzymes/acids, gastrointestinal motility, recruitment of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient or enzymes, gastrointestinal professes may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33 goonists, antagonists and ligands and to produce antibodies
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                              Zaig13; gastric motility; gastrointestinal inflammation; reflux disease; nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                                                                                          Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility.
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Pred. No. 3e-14;
0; Mismatches
                                                                                              1. .23
/note= "signal peptide"
                                                                                                                              /note= "mature protein"
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                                                                                   Location/Qualifiers
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88.6%;
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          Protein designated zsig33.
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                                                                 Homo sapiens
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human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be associated with decreased activity or function of HSPP. Antagorists of HSPP are used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagorists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosolerosis, circhosis, psoriasis, acquired immune deficiency syndrome, anaemia, circhosis, psoriasis, acquired immune deficiency syndrome, anaemia, circhosis, disease, Alaheimer's Parkinson's or Huntington's disease, Alaheimer's Parkinson's or Huntington's disease, Alaheimer's Parkinson's or Huntington's cischaemic heart disease, Alaheimer's Parkinson's or Huntington's disease, activophrenia, ovulatory defects, muscular dystrophy). HSPP, conclete acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming cribbentics, for detecting related sequences or genetic variations, and for chromosomal mapping HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists of potential therapoutic agents of the used to raise specific antibodies (Ab) and to screen for agonists and antagonists of potential therapoutic agents of the used to raise and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural
Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; calribosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alizheimer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baughn MR;
8, Hillman JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley NC, Guegler KJ, Ba
H, Patterson C, Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP
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98US-0094983P.
98US-0102686P.
98US-0112129P.
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Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.6
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-160673/14.
                                                                                                                                                                                                                                                                                                                                        muscular dystrophy
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Akerblom IE,
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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24. 37 /note= "specifically claimed fragment that binds to the GHS-R"

Location/Qualifiers

Homo sapiens

Peptide

gastric contractility; nutrient uptake; digestive; pancreatic, human; insulin-like growth factor-I; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R; G-protein coupled receptor.

hormone; enzyme; neural development;

zsig33; signal transduction;

Human zsig33 polypeptide.

(first entry)

23-JUL-2001

AAB62649;

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The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP is a ligand for growth hormone secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum tissue, modulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating gastric
                                                                                                                                               SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue; therapy;
                                                                                                                                                                                                                                                                                                              24. .34
/label= SGIP_peptide
/note= "this peptide is claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishop PD;
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88.6%; Pred. No. 3e-14;
iive 0; Mismatches
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                                                                                                                                                                                                                                                      l. .23
/label= Signal_peptide
                                                                                                                                                                                                                                                                                 24. .117 _____/label= Mature_protein
                                                                                                                                                                                                                                        Location/Qualifiers
                            AAB20101 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; 54; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SR,
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jaspers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-123010/13.
N-PSDB; AAF30033.
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tes 39; Conserv
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                                                                                                                   Zsig33 protein
                                                                                                                                                                                                                                                                                                                                                                          WO200100830-A1
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                                                                                                                                                                                                          Homo sapiens
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                                                                                     23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-2001
                                                        AAB20101;
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                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                             human.
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Matches
          AAB2010
RESULT
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Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide.

Claim 1; Page 93-94; 111pp; English.

PD;

Bishop

Deisher TA,

Jaspers SR,

Sheppard PO,

WPI; 2001-355879/37. N-PSDB; AAF83678.

(ZYMO ) ZYMOGENETICS INC

22-NOV-2000; 2000WO-US032074.

WO200138355-A2.

31-MAY-2001

99US-0166765P

22-NOV-1999;

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The invention relates to a method of forming a reversible peptide-
c receptor complex that involves providing an immobilized receptor, and
c contacting the receptor with a zsig33 peptide (Comprising residues 24.37
c of AABG6549), where the receptor binds to the zsig33 peptide. The method
is useful for purifying cells, purifying a peptide, stimulating signal
c transduction in a cell expressing a receptor. It is also useful for
modulating secretion of hormones, neural development and/or utilization,
c gastric contractility, nutrient uptake, secretion of digestive and
c gastric contractility, nutrient uptake, secretion of insulin-like growth factor
c j secretion of non-zsig33 proteins. It is useful for modulating growth
c hormone secretion in a mammal having a disease associated with abnormal
c hormone secretion in a mammal having a disease associated with abnormal
c remodeling, low osteoblast levels, cartilage repair and remodeling,
skeletal dysplasia, immune suppression, obesity, growth retardation,
c protein catabolic responses after surgery, cachexia, protein loss,
c protein catabolic responses after surgery, cachexia, protein loss,
c martism, wound healing and ovulation induction, treating a mammal having
a metabolic disorder requiring neurological feedback, such as satiety
c regulation, glucose absorption and metabolism and neuropathy-associated
c gastrointestinal disorders, and stimulating glucose-induced insulin
c release in a mammal. The present sequence represents the human zsig33
c polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pred. No. 3e-14;
0; Mismatches 5; Indels
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88.6%;
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Best Local Similarity 88.6
Matches 39; Conservative
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MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP

ID AAB62649 standard; protein; 117 AA

AAB62649

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroals; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, Wa
Zhang J,
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Yang Y,
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Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; SEQ ID NO 2035; 10078pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rman T, Xu C,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as central nervous system injuries.
                                                             AAM38890 standard; protein; 117 AA
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                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-0048775.
25-APR-2000; 2000US-0052317.
20-JUN-2000; 2000US-00599042.
19-JUL-2000; 2000US-00620312.
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14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
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Wang Z, Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WO-US034263
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                                                                                                                                                                                       (first entry)
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Goodrich R,
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                                                                                                                                                                                    22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia
                                                                                                                       AAM38890;
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Zhou P,
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RESULT 8
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also mocimpasses the unmodified peptides; the DNA encoding the peptides.

The invention and no season peptides in the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention, and an assay and kit for detecting the peptides. The peptides caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth chormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide compounds which induce growth hormone secretion and elevate calcium concentrations, useful in treatment and diagnosis of infant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                          Growth hormone secretagogue, GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.9%; Score 198; DB 4; Length 117; 88.6%; Pred. No. 3e-14; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPSPGTVCSLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsuo H,
                                                                                                                                   Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 182; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hosoda H,
                              AAB60511 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                             24-JUL-2000; 2000WO-JP004907.
                                                                                                                                                                                                                                                                                                                                                                          23-JUL-1999; 99JP-00210002
29-NOV-1999; 99JP-00338841
26-APR-2000; 2000JP-00126623.
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159704/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 117 AA;
                                                                                                                                                                                                                                                                        WO200107475-A1.
                                                                                                 24-APR-2001
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                           01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kangawa K,
                                                                AAB60511;
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Matches
              AAB60511
ID AAB
RESULT
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Query Match . 31.9%; Score 198; DB 4; Best Local Similarity 88.6%; Pred. No. 3e-14; Matches 39; Conservative 0; Mismatches

RESULT 10 ABB78319

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Gaps

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4; Length 117; 5; Indels

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nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate 2SIG33 expression.

The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The 2SIG33 mod in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and also used as diagnostic agents for detecting the production of antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assay (BLISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zero and zero in gene therapy. The present sequence is and zsig33-like DNA is used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to zsig33-like peptides and their corresponding
                      Human, 28ig33-like peptide; gastric contractility, nutrient uptake, growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 198; DB 5; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3e-14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 27; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE15883 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                11-MAY-2000; 2000US-0203300P
                                                                                                                                                                                                                                       10-MAY-2001; 2001US-00853253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                        JASPERS S R.
SHEPPARD P O.
DEISHER T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zsig33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-443750/47.
                                                                                                                                                                                                                                                                                                                                                                                          BISHOP P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD38238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 117 AA;
                                                                                                                                                    US2002055156-A1
                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaspers SR,
                                                                                                                                                                                             09-MAY-2002
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                                                                                                                                                                                                                                                                                                                             (JASP/)
                                                                                                                                                                                                                                                                                                                                                                                            (BISH/)
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(DEIS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP SGIP and an assays to identify modulators of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antianishes may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used as diagnostic agents for detecting the presence of SGIP in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                           Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deisher TA,
                                                                                                                                                                                                                                                                                       .. .23
'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                 /note= "mature protein"
                                                                                                                                Amino acid sequence of a human zsig33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 39-40; 23pp; English.
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
ABB78319 standard; protein; 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000US-00608810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0141592P
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                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human zsig33 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117 AA;
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            US6420521-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1999;
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                                             ABB78319
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                                                                                                                                                                                                                                                                                Peptide
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Bishop PD;

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Gaps

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5; Indels

Best Loca Matches

ò 셤 RESULT 11 AAE23838

EXAXAX

Mark Control

ABU58046

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The invention relates to zsig33-like peptides (ZS33LP) including zsig33-CC linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon control peptides and nucleic acid molecules encoding such zsig33-like peptides. ZS33LP peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients auch as human immunodeficiency virus (HIV) patients, in improving vaccines and in the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other contentiation in the liver, blood vessel formation and other compendent processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic chypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic chypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic corpusations containing glucose and as adsorption enhancers for the insulin release. They are also useful as research reagents for cell-cell interactions of tissues associated with gastrointestinal and growth captened of insulin releases. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and growth creating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth created diseases. Z633LP peptides, nucleic acids and/or antibodies are contractility, secretion of digestive enzymes, inflammation and regulation contractility, recruitment of digestive enzymes, inflammation and regulation of contractility, and digestive enzymes, inflammation and acids, contractility, accruitment of digestive enzymes, inflammation and acids, contractility, accruitment of digestive enzymes, inflammation and acids, contractility ande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like
Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
adsorption enhancer; gastrointestinal disease; growth related disease;
inflammation; gene therapy; growth regulation; blood vessel formation;
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                                                                                                                                                                                                                                                                                             /note= "Human mature zsig33 protein"
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                                                                                                                                                                                                                        1. .23
/label= Signal_peptide
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                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000; 2000US-00569271.
                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2001; 2001WO-US015091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC
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N-PSDB; AAD25759.
                                                                                                    HIV; zsig33 protein.
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                                                                                                                                                                                                                                                                                                                                              WO200187933-A2.
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides.
                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                      Protein
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stomach; liver;
                                                           Human; PRO; cytostatic; tumour; cancer; breast; lung; e
horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
ABU58046 standard; protein; 117 AA.
                                                                                                                                                                                                                98US-0078910P.
98US-0083322P.
98US-0084600P.
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98US-0088028P.
98US-0088029P.
98US-0088030P.
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97US-0065311P.
97US-0066770P.
98US-0075945P.
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98US-0088217P.
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                              (first entry)
                                             Human PRO polypeptide #78
                                                                                                           US2003027163-A1
                                                                                            Homo sapiens.
                                                                                                                                           15-NOV-2001;
                             14-APR-2003
                                                                                                                                                                                                                                        28-MAY-1998;
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               ABU58046;
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0; Gaps

31.9%; Score 198; DB 5; Length 117; 88.6%; Pred. No. 3e-14; ive 0; Mismatches 5; Indels

Best Local Similarity 88.6 Matches 39; Conservative

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Query Match

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98US-0089947P
98US-0089947P
98US-0089947P
98US-0089952P
98US-0090254P
98US-0090254P
98US-0090254P
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98US-0090254P
98US-0090254P
98US-0090444P
98US-0090444P
98US-0090444P
98US-0090652P
98US-009069B
 19 - JUN - 1998

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ABU59124;

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Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; endothelial growth factor inhibition; VEGF inhibition; endothelial growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; meanmalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                            Novel human secreted or transmembrane protein PRO1066
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9705-006521BP
9705-0065311P
9705-0065311P
9805-0075945P
9805-0075945P
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                                                                                                                                                            Homo sapiens.
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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO928, PRO926, PRO1069 or PRO535, PRO1060 or PRO535, PRO1060 or pRO535, PRO1060 or disorders where angiogenesis would be useful for treating conditions or disorders where angiogenesis would be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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Godowski P
Paoni NF;
Wood WI;
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            98WO-US019330.
98WO-US019437.
98WO-US021141.
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99WO-US000106.
99WO-US005028.
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99WO-US021090.
99WO-US021547.
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09-JUL-2001; 2001WO-US021735.
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          beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PROB12 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting tumour growth. PROB26, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PROB26, PRO10182 is also enhances survival/proliferation of retinal neurons cells (PRO1132 is also enhances survival/proliferation of redinal neurons cells (PRO1132 is also enhances survival/proliferation of redinal neurons cells (PRO1132 is also enhances survival/proliferation of isorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with dermatitis, herpetiformis or Crohr of disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.
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30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
30 - JUL - 1998,
04 - AUG - 1998,
10 - AUG - 1998,
                                                                                                                                             10-AUG-1998
11-AUG-1998
11-AUG-1998
17-AUG-1998
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10-MAR-2000; 2000WO-US005841.

15-MAR-2000; 2000WO-US006819.

15-MAR-2000; 2000WO-US006819.

30-MAR-2000; 2000WO-US01377.

31-MAY-2000; 2000WO-US01378.

17-MAY-2000; 2000WO-US01378.

30-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000WO-US01524.

30-MAY-2000; 2000WO-US01524.

32-MUN-2000; 2000WO-US01524.

23-JUN-2000; 2000WO-US01524.

23-JUN-2000; 2000WO-US01524. 셤 ઠે

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Search completed: July 11, 2006, 17:00:15 Job time : 196 secs

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 11, 2006, 17:00:33 ; Search time 39 Seconds (without alignments) 288.650 Million cell updates/sec

US-10-659-782B-32 620 Title: Perfect score:

1 MPSPGTVCSLLLLGMLWLDL.......PPSSRERSRRSHQPSCSPEL 117 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

, and a second	Description	dhrelin precursor	ghrelin precursor	regulator of nucle	hypothetical prote	anti-mullerian hor	D3	hypothetical prote	hypothetical prote	thyrotropin recept	lyase - Pseudomona	interleukin-1beta	unknown protein Fl	probable membrane	hypothetical prote	retrotransposon li	hypothetical prote	thyrotropin recept	hypothetical prote	sensor protein Bas	sensor protein for	sensor protein bas	hypothetical 51.8K	probable MYB famil	interleukin-1beta	interleukin-1beta	conserved hypothet	site-specific DNA-	hypothetical prote	
SUMMAKIES	QI	A59316	B59316	AG0449	T34274	JC4335	E64211	H83043	T22943	I48882	S77905	A56084	H96792	S62048	T32425	B85188	E71436	A35956	T51876	F91265	C86106	JX0285	C39926	G84707	C56084	B56084	A75560	JH0634	T28897	S25080
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de	Query	31.9	25.5	12.6	11.9	11.8	11.8	11.7	11.6	11.5	11.4	11.4	11.1	11.1	11.0	11.0	11.0	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.6	10.6	10.6
	Score	198	158	78	73.5	73	73	72.5	72	71.5	70.5	70.5	69	69	68	68	69	67.5	67	67	67	67	67	67	66.5	66.5	66.5	99	99	65.5
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hypothetical prote conserved hypothet	hypothetical prote regulatory protein	mitosis initiation hypothetical prote	ABC transporter, A	serine proteinase	probable transmemb	hypothetical prote	fission yeast Skb1	mitosis initiation	sensory transducti	titin - rabbit (fr	ribosomal protein	hypothetical prote
T33503 B64187	S16506 S32932	A38436 T19507	G75548	S45493	T36589	T27400	T03842	T13648	877175	S20901	A57296	T19409
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307	381 415	708 188	354	467	502	540	637	695	749	6805	221	746
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65.5	64.5 64.5	64.5 64	64	64	64	64	64	64	64	64	63.5	63.5
30	33	ა ი გ ი	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

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Cispecies: Homo sapient (man)
Cispecies: Homo sapient (man)
Cispecies: Homo sapient (man)
Cipate: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
Cipate: 16-Jun-2000
Cicatesion: A59316
Cipate: 16-Jun-2000
Cispecies: Homo sapient (man)
Cipate: 16-Jun-2000
Cispecies: Man, Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A; Homomer: A59316
A; MUD:20067959; PMID:10604470
A; Reference number: A59316; MUD:20067959; PMID:10604470
A; Reference number: A59316
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A; Residues: In-117 < ROJ>
A; Residues: 1-117 < ROJ>
A; Residues: 1-117 < ROJ>
A; Residues: UNIPROT:Q9UBU3; UNIPARC:UP100000362D3; GB:AB029434; NID:g6691571; PA; Experimental source: tissue stomach endocrine cells
A; Note: submitted to GenBank, June 1999
C; Superfamily: motilin secreted by the stomach stimulates the release of somatotropin (grow Cisperfamily: motilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;2-21/Domain: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CT
F;26/Binding site: octanoate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 198; DB 1; Length 117;
Pred. No. 1.7e-13;
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88.6%;
ghrelin precursor - human
N;Alternate names: preproghrelin
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Best Local Similarity
Matches 39; Conserva
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5; Indels 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44 0; Mismatches 39; Conservative

1 MPSPGTVCSLLLLGMLWLDLAWAGSSFLSPEHQRVQQRKESKKP 44 g ò

ghrelin precursor - rat

NyAlternate names: preproghrelin

Cispecies: Rattus norvegicus (Norway rat)

Cibate: 16-Unn-2000 Hesquence\_revision 16-Jun-2000 #text\_change 09-Jul-2004

Cibate: 16-Unn-2000 Hesquence\_revision 16-Jun-2000 #text\_change 09-Jul-2004

Cibate: 16-Unn-2000 Hesquence\_revision 16-Jun-2000 #text\_change 09-Jul-2004

Cibate: 16-Unn-2000 Hesquence\_revision 16-Jun-2000

Cibate: 16-Unn-2000 Hesquence\_revision 16-Jun-2000

Cibate: 16-Jun-2000 Hesquence 09-Jul-2004

Airtile: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

Airtile: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A, Steaus: DS316
A, Status: not compared with conceptual translation
A, Status: not compared with conceptual translation
A, Molecule type: mRNA protein
A, Residues: 1-117 < KOA)
A, Cross-references: UNIPROT: Q9QYH7; UNIPARC: UPI000012B411; GB: AB029433; NID: g6691569;
A, Experimental source: strain SD; tissue stomach endocrine cells

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A, Map position: X
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T4) The sequence of C. elegans cosmid F46H5.
The sequence of C. elegans cosmid F46H5.
The sequence of C. elegans cosmid F46H5.
T34274
T
A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt C;Comment: Ghrelin secreted by the stomach C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAIP
F;24-51/Product: ghrelin #status propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVSSATICSLILLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP-----PAKLQPRALE
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                                                                                                                                                                                                                                                                                                                                                            Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
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                                                                                                                                                                                                                                                                                                                                                                Score 158; DB 1;
Pred. No. 2.5e-09;
                                                                                                                                                                                                                                                                                                                                   25.5%; bcc. No. 2...
40.0%; Pred. No. 2...
7; Mismatches
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Best Local Similarity
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A;Introns: 16/2; 52/3; 87/2; 116/2; 138/2; 203/1; 265/3; 317/2; 337/3; 378/1; 428/1; 482
7/3; 1491/3; 1560/2; 1632/2; 1753/3; 1830/2; 1862/2; 1927/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-mullerian hormone type II receptor precursor - human C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Jate: O6-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C.Accession: JC4335
R;Visser, J.A.; McLuskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegoedla shochem. Biophys. Res. Commun. 215, 1029-1036, 1995
A.Title: Structure and chromosomal localization of the human anti-muellerian hormone type A;Reference number: JC4335; MUID:96028015; PMID:7488027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-573 <VIS>
A,Cross-references: UNIPROT:Q16671; UNIPARC:UPI000016A54B; GB:X91156; NID:g1107671; PIDN
C,Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a cri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Dates: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Proser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.,
M.; Puhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.C.A.; Ventex, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:696210; OMIM:600956
A;Amp position: 12q13-12q13
A;Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
A;Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C;Keywords: ATP; hormone receptor; transmembrane protein
F;1-6/Domain: signal sequence #status predicted <SIG>F;17-573/Product: anti-muellerian hormone type II receptor #status predicted <MAT>F;17-141/Domain: extracellular hormone binding #status predicted <ELB>F;142-167/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                         95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGTVCS-------LLLLGMLWLDLAMAGS---SFLSPEHQRVQVRP-PHKAP
                                                                                                                                                                                                                                         38 RPPHKAPHVVPALPLSNOLCDLEOORHLWASVFSOSTKDSGSDLTVS--GRTWGLRVLNR
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                     652 RTPHFTDEIKLSLP----CDLNDGHHLLFTVYHISCKEGDSSSTESPIGYTW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                  Indels 17;
                                                                                                      Length 2018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virulence-associated protein vacB homolog - Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 573;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Indels
                                                                                                                                                                  31;
                                                                                                      DB 2;
                                                                                               Score 73.5; DI
Pred. No. 37;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 11.8%; Score 73; DB 1 Similarity 27.4%; Pred. No. 10; 34; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            96 LFP--PSSRERSRRSHQPSC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                        700 -LPLYRNGKLRSGNFHLPVC 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : || :||
188 DSGRDWSVELQELP---ELC---
                                                                                               Query Match
Best Local Similarity 31.2%;
Matches 25; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPSS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPRS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: AMHR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٣
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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S.

Length 666;

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C; Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C; Accession: 148882
E; Stein, S.A.; Oates, E.L.; Hall, C.R.; Grumbles, R.M.; Fernandez, L.M.; Taylor, N.A.;
Mol. Endocrinol. 8, 129-138, 1994
A; Title: Identification of a point mutation in the thyrotropin receptor of the hyt/hyt i
A; Reference number: A54271; MUID:94224232; PMID:8170469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: I48882
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-764 mRS>
A;Cross-references: UNIPROT:P47750; UNIPARC:UPI0000003F87; EMBL:U02602; NID:9575923; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyase - Pseudomonas pseudomallei
C;Species: Pseudomonas pseudomallei
C;Species: 21-Apr-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: 877905; 836445; 836446
R;Penaloza-Vazquez, A.; Mena, G.L.; Herrera-Estrella, L.; Bailey, A.M.
A;Penaloza-Vazquez, A.; Mena, G.L.; Herrera-Estrella, L.; Bailey, A.M.
A;Title: Cloning and sequencing of the genes involved in glyphosphate utilization by Ps
A;Reference number: 877905; MUID:96031567; PMID:7574593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-309 <PEN>
A;Cross-references: UNIPROT:Q52502; UNIPARC:UPI0000B6398; EMBL:X74325; NID:g439726; PI
A;Experimental source: strain 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Gene: TSHr
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
C;Superfamily: glycoprotein hormone receptor; transmembrane protein
F;S3-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
                                                                                                                                                                                                                                                                    3 PGSL--LLLVLLLALSRSLRGKECASPPCECHQEDDFRVTCKELHRIPSLPPSTQTLKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PGTVCSLLLLGMLWLDLAMAGSSFLSPE---HQRVQVRPPHKAPHVVPALPLSNQLCDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thyrotropin receptor precursor - mouse
N;Alternate names: thyroid-stimulating hormone receptor; TSH receptor
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QQ--RHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 ORVOVRPPHKAPHVVPALPLSNQLCDLEQQR-HLWASVFSQSTKDSGSD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Indels
A;Gene: CESP:F58G11.3
A;Map position: 5
A;Introns: 42/2; 82/2; 153/3; 274/3; 380/1; 569/3; 613/3
                                                                                                                 Query Match 11.6%; Score 72; DB 2; Best Local Similarity 26.9%; Pred. No. 16; Matches 32; Conservative 11; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 71.5; 28.8%; Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                    81 LTVSGRTWGLRVLNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 28.89
Matches 32; Conservative
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                                                                                                  A;Cross-references: UNIPROT: P47350; UNIPARC:UP100001344B5; GB:U39690; GB:L43967; NID:gld
A;Experimental source: strain G-37
G;Genetics:
A;Genetics:
C;Superfamily: virulence-associated protein vacB homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypotherical protein F58G11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22943
R;Percy, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19640
A;Reference number: Z19640
A;Reference number: DNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-666 < WLL>
A;Residues: 1-666 < WLL>
A;Cross-references: UNIPROT:P90898; UNIPARC:UPI000007850D; EMBL:Z81094; PIDN:CAB03154.1;
A;Experimental source: clone F58G11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 LYVAIADVAHYVNRNSEIDIEAKHKTSSIYLPGHYVVPMLPEQLSNQLCSLNPAQKRYVV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 SLLPLAMRWAGRSRAGSEF---ELGRM------LPLQ---AVIEESLHLAIS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLEQQRHLWAS 68
                                 not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pothetical protein PA4822 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                               18 LDLAMAGSSFLSPEHQRVQVRPPHKAP-----HVVPALP--LSNQLCDLEQQRHLWAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72.5; DB 2; Length 555; Pred. No. 11; 9; Mismatches 34; Indels 29
                                                                                                                                                                                                                                                                                          ; DB 1; Length 725;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NKLYPATIISKNRFSY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 VFSQSTKDSGSDLTVSGRTWGLRVLNRLPPPSSRERSRRSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 VFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 AFLREDLDAALRLVAR----KKLLQRLEADASRERFRR 493
                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                          Query Match
11.8%; Score 73; DB 1
Best Local Similarity 25.7%; Pred. No. 14;
Matches 26; Conservative 16; Mismatches
                              preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.3%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 VCEISFDNOGRIKT-
                     A Status: preliminary; nu
A; Molecule type: DNA
A; Residues: 1-725 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: H83043
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Gaps

13;

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A;Cross-references: UNIPROT:Q9C9K7; UNIPARC:UPI00000A0BE5; GB:AE005173; NID:g6642668; PI.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1487 <BRU>
A;Residues: 1-1487 <BRU>
A;Cross-references: UNIPARC:UPI000052E6A; EMBL:Z72719; NID:g1322824; PID:e243500; PID:grapherimental source: strain $288C C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1487 <KLI>
A;Cross-references: UNIPROT:P53094; UNIPARC:UPI0000052E6A; EMBL:X91837; NID:g1177627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain FY1679
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, submitted to the Protein Sequence Database, May 1996
A;Reference number: S64183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YGL197w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G1307
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S62048; S64214
R;Klima, R.; Coglievina, M.; Bertani, I.; Zaccaria, P.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A;Reference number: S62045
A;Accession: S62048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSISEAEHOR-----RASHPLTSSPLFEDSGTPCGKOLOOLOOHTIONPHNHLSPRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSFLSPEHORVOVRPPHKAPHVVPALPL-----SNOLCDLEQ-----QRHLWASVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PELHHQLQPQPQLHPLPQPQPQPQPQQQNSDDE-----SDSNKDPGSDPVTSGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 PE-HQRVQVRPP-HKAPHVVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRT
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
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                                                                                                                                                                                                                                                                                                                                      Length 302;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Map position: 7L

X,Reywords: transmembrane protein

F;1034-1056/Domain: transmembrane #status predicted <TM1>

F;1052-1068/Domain: transmembrane #status predicted <TM2>
   A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 WGLRVLNRLFPPSSRERSR-------RSH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 -GKRPRGR--PPGSKNKPKPPVIVTRDSPNVLRSH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 69; DB 2; 25.7%; Pred. No. 78; ive 10; Mismatches 37
                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                   Score 69; DB
Pred. No. 13;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: SGD:S0003165; MIPS:YGL197w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 905
                                                                                                                                                                                                                                                 A, Map position: 1
C, Superfamily: AT-hook DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              882 MSTGSNTRRSNTLTDYMHSNKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RSRRS-----HQPSCSP
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.6%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                      A, Accession: H96792
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-302 <STO>
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nes 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S64214
                                                                                                                                                                                                           A;Gene: F14G6.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SGD: MDS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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Matches
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Cydcession: ASG084
Cydcession: ASG084
Cydcession: ASG084
Cydcession: ASG084
Cydrides: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Chosener in Ayritle: Cydenetics:

Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of four novel isoforms of human interleukin-lbeta convex Ayritle: Cloning and expression of human interleukin-lbeta convex Ayritle: Cloning and expression of human interleukin-lbeta convex Ayrit
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H96792
Unknown protein F14G6.10 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C; Accession: H96792
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Anture 408, 816-820, 2000
A; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Athchors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vencer, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                   54 NQLCDLEQQRHLWASVFSQSTKDSGSDLT-----VSGRTWGL----RVLNRLFP
                                                                                                                                                                                                                                             2 PSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPH--------VVPALPLS
                                                                                                                                                                                                                                                                                                       ----LSGVHKSRRGRPPQKAAYLARWKYSPIVAADPRA
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                 51;
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                                                                                                                           Length 309;
                                                                                                                                                                                    Indels
                                                                                                                                                                              36;
                                                                                                                        DB 2;
                                                                                                     Score 70.5; DF
                                                                                                           11.4%; Score ... 22.0%; Pred. No. 9.6;
                               A,Gene: glpB
C,Superfamily: Pseudomonas pseudomallei lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLCDLEQQRHLW----ASVFSQSTKDS----
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Best Local Similarity 22.0%
Matches 27; Conservative
                                                                                                                  Query Match
Best Local Similarity 22.0°
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 PSSRERSRRSHQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 RKSLNAAKPSHR 117
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QNL 175
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C;Genetics:
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C. Accession: T32425
R. Wohldmann, P.; Sansone, J.
A. Reserved on the EMBL Data Library, September 1997
A. Reference number: Z21165
A. Reference number: Z21165
A. Reference number: Z21165
A. Reference number: Z21165
A. Reserved on the EMBL Data Library, translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residue: Lype: DNA
A. Residue: Lype: DNA
A. Residue: Lype: DNA
A. Experimental source: strain Bristol N2; clone C1062
C. Genetics:
A. Genetics:
A. Genetics:
A. Genetics:
A. Map position: X
A. Introns: 85/2; Z20/2; 269/1; 305/1; 519/3; 576/3; 724/3; 755/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retrotransposon like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85188
C;Accession: B85188
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Accession: B85188
A;Accession: B85188
A;Accession: B8188
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-1474 <STO>
A;Residues: 1-1474 <STO>
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 LSLANSLTWLLSSSNGNLSVPQTPTKEHH--PTAPTSNRKCDLPRSN---STTISQLTKD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 LDLAMAGSSFLSPEHORVQV-RPPHKAPHVVPALPLSNOLCDLEOORHLWASVFSOSTKD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 LWLDLAMAGSSFL--SPEHQRVQVRPPHKAPHVV---PALPLSNQLCDLEQQRHLWASVF 70
hypothetical protein C10E2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.0%; Score 68; DB 2; Length 796; Best Local Similarity 28.6%; Pred. No. 50; Matches 28; Conservative 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Indels
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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065WJ7_9AVES

0674B4_TRASC

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067WJ5_DRONO

067WJ6_MARPL

052B56_BACSU

0458B46_TETNG

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0458B46_TETNG

045B401_YERPE

03CWJ7_YERPE

03CWJ7_YERPE
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License EMBL; AY184207; AA027351.1; -; mRNA.
Ensembl; ENSG0000157017; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
GO; GO:0016091; P:regulation of physiological process; IEA.
InterPro; IPR00541; Preproghrelin.
PANTHER; PTHRILI2; Preproghrelin; 1.
Pfam; PF04644; Motilin ghrelin; 1.
PRINTS; PR01624; GHRELIN. Jeffery P.L., Herington A.C., Chopin L.K.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. 91 AA; 9972 MW; E7E532D32A3F8609 CRC64;

; Score 198; DB 2; Length 91; Pred. No. 1.3e-12; 0; Mismatches 5; Indels 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAP

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Gaps

1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP

GHRL HUMAN STANDARD; PRT; 117 AA.
QUUBUJ; QBTAT9; Q9H3R3;
13-DEC-2001, integrated into UniProtKB/Swiss-Prot.
01-MAY-2000, sequence version 1.
07-MAR-2006, entry version 52.
Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) (M46 protein) (Contains: Ghrelin-27; Ghrelin-28 (Ghrelin); Obestatin).
Name-GHRL; Synonyms-MTLRP; ORFNames=UNG524/PRO1066;

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MEDINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XX MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Romstein M.J. Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Redriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Bukeeley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WUCLEOTIDE SEQUENCE [LARGE SCALE MENA] (ISOFORM 1).

WICLEOTIDE SEQUENCE [LARGE SCALE MENA] (ISOFORM 1).

WICLEOTIDE SEQUENCE [LARGE SCALE MENA] (ISOFORM 1).

A Clark H.F., Gurney A.L., Abaya E. Baker K., Baldwin D.T., Brush J.,

Chow B., Chow B., Chim. C., Crowley C., Currell B., Deuel B., Dowd P.,

Baton D., Foster J.S., Grimaldi C., Gu O., Hass P.E., Heldens S.,

Huang A., Kim H.S., Kilmowski L., Johnson S., Lee J.,

A Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R.L., Wateranabe C., Wieand D., Woods K., Xie M.-H.,

A vandlen R.L., Wateranabe C., Wieand D., Woods K., Xie M.-H.,

A vandlen R.L., Wateranabe C., Wieand D., Woods K., Zhang Z., Goddard A.D.,

Nood W.I., Godowski P.J., Gray A.M.;

The secreted prorein discovery initiative (SPDI), a large-scale

XT effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Stomach;
PubMed=1214(4009; DOI=10.1074/jbc.M205366200;
PubMed=1214(4009; DOI=10.1074/jbc.M205366200;
Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
"Structural divergence of human ghrelin. Identification of multiple
"Structural divergence of human ghrelin. Identification of multiple
ghrelin-derived molecules produced by post-translational processing.";
J. Biol. Chem. 278:64-70(2003).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 2), TISSUE SPECIFICITY, ACYLATION OF SER-26, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                 Kangawa K.;
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=2038976; PubMed=10930375;
Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
"Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";

Gastroenterology 119:395-405 (2000).
                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND ACYLATION OF SER-26
                                                                                                                                                                                                              Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kanga<sup>,</sup>
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                  MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leibel R.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wajnrajch M.P., Ten I.S., Gertner J.M., Leibel R.L. "Genomic organization of the human Ghrelin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocr. Genet. 1:231-233 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                         Nature 402:656-660(1999).
                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Stomach
                                                                                                                                                                                                                                                                stomach.
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-!- MASS SPECTROMETRY: MW=3398.9; MW ERR=0.3; METHOD=Electrospray;
RANGE=44-51 (Ghrelin-28-C10); NOTE=0-decanoylated form (Ref.4).
-!- MASS SPECTROMETRY: MW=3397.2; MW ERR=0.5; METHOD=Electrospray;
RANGE=24-51 (Ghrelin-28-C10:1); NOTE=0-decanoylated form (Ref.4).
-!- MASS SPECTROMETRY: MW=3371.3; MW ERR=0.1; METHOD=Electrospray;
RANGE=24-51 (Ghrelin-28); NOTE=0-octanoylated form (Ref.4).
-!- MASS SPECTROMETRY: MW=3243.6; MW ERR=0.4; METHOD=Electrospray;
RANGE=24-50 (Ghrelin-27-C10); NOTE=0-decanoylated form (Ref.4).
-!- MASS SPECTROMETRY: MW=3214.6; MW ERR=0.6; METHOD=Electrospray;
RANGE=24-50 (Ghrelin-27); NOTE=0-decanoylated form (Ref.4).
-!- SIMILARITY: Belongs to the motilin family.
-!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/GhrelinID327.html".
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=Ghrelin; Named isoforms=2; Name=1; Synonyms=Ghrelin; Isold=Oybu3-1; Sequence=Displayed; Isold=Oybu3-1; Sequence=Displayed; Name=2; Synonyms=del-Gln14-ghrelin; Isold=Oybu3-2; Sequence=VSP 003245; Isold=Oybu3-2; Sequence=VSP 003245; TISSUE SPECIFICITY: Highest level in stomach. All forms are found in serum as well. Other tissues compensate for the loss of ghrelin synthesis in the stomach following gastrectomy. PTM: O-n-octanoylation is essential for ghrelin activity. The O-n-decanoylated forms Ghrelin-27-C10 and Ghrelin-28-C10 differ in the length of the carbon backbone of the carboxylic acid bound to Ser-26. A small fraction of ghrelin, ghrelin-28-C10:1, may be modified with an unsaturated carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3; Kojima M., Hosoda H., Matsuo H., Kangawa K.; "Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induces adiposity and stimulates gastric acid secretion. Involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 66 of January 2006; WWW="http://www.expasy.org/spotlight/back_issues/sptlt066.shtml".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in growth regulation.
PUNCTION: Obseratin is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal motility (By similarity).
SUBCELLULAR LOCATION. Secreted protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Ghralin is a specific ligand for the growth hormone
secretagogue receptor type I (GHSR) inducing the release of gro
hormone from the pituitary. Has an appetite stimulating effect,
                                                                                                                                              PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; Signal peptide prediction based on analysis of experimentally verified cleavage sites."; Protein Sci. 13:2819-2824(2004).
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL; AJ55278; CAB65733.1; -; mRNA.
EMBL; AF286558; AAG10300.1; -; Genomic_DNA.
EMBL; AB035700; BAB19045.1; -; mRNA.
EMBL; AX358053; AAQ89412.1; -; mRNA.
EMBL; BC025791; AAH25791.1; -; mRNA.
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PDB; 1P7X; Model; A=1-117.

Ensembl; ENSG00000157017; Homo sapiens.

H-InvDB; HIX0003050; -.

HGNC; HGNC: 18129; GHRL.

MIM; 605353; gene.
                                                                                                                  PROTEIN SEQUENCE OF 24-38
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                      /FTIG=PRO 0000019202.
Ghrelin-27
/FTIG=PRO 0000019203.
FEROVed in mature form.
/FTIG=PRO_000019204.
Obestatin (By similarity).
/FTIG=PRO_000045140.
Removed in mature form (By similarity).
/FTIG=PRO_000045141.
/FTIG=PRO_000045141.
                                                        .; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and form ghrelin-28-C10).
O-octanoyl serine (in form ghrelin-27 and
form ghrelin-28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-decanoyl serine (in form ghrelin-27-C10
GO; GO:0005615; C:extracellular space; ISS.

GO; GO:001664; F:G-protein-coupled receptor binding; ISS.

GO; O001669; F:G-protein-coupled receptor binding; ISS.

R GO; GO:00186; F:G-protein coupled receptor protein signalin. .; I.

R GO; GO:0050791; P:regulation of physiological process; ISS.

InterPro; IPR006737; motilin_assoc.

InterPro; IPR006737; motilin_assoc.

InterPro; IPR006741; Preproghrelin.

R Pfam; PF04644; Motilin_assoc.

R ProDom; PD32162; Preproghrelin; 1.

R ProDom; PD32162; Preproghrelin; 1.

R Direct protein sequencing; Hormone; Lipoprotein; Signal.

I SIGNAL
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Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
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QGUDE7;
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Matches 39; Conservative
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                    EMBL; AY372274; AAQ74837.1; -; Genomic_DNA.

R EMBL; AY372274; AAQ74837.1; -; mRNA.

R GO; GO:0005576; C:extracellular region.

R GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.

GO; GO:0057091; P:regulation of physiological process; IEA.

R InterPro; IPR006737; motilin_assoc.

InterPro; IPR006738; motilin_assoc.

InterPro; IPR006738; motilin_assoc.

InterPro; IPR006741; Preproghrelin.

R PANTHER; PTHR14122; Preproghrelin; 1.

Pfam; PF04644; Motilin_assoc; 1.

R Pfam; PF04644; Motilin_assoc; 1.

R PRINTS; PR01624; Motilin_assoc; 1.

R PRODOM; P0332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Ensembl; ENSG0000157017; Homo sapiens.
Go, GO:0005576; C:extracellular region; IEA.
GO; CO:0015608; F:growth hormone-releasing hormone activity; IEA.
InterPro; IPR00541; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
influencing ghrelin gene expression and fasting plasma levels.";
Endocrinology 145:2197-2205(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15604212; DOI=10.1210/en.2004-1306; Wei W., Wang G., Qi X., Englander E.W., Greeley G.H. Jr.; "Characterization and regulation of the rat and human ghrelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 194; DB 2; Length 117;
Pred. No. 4.7e-12;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 187; DB 2; Length 36;
Pred. No. 6.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-2004, integrated into UniProtKB/TrEMBL. 23-NOV-2004, sequence version 1. 07-FEB-2006, entry version 7. Ghrelin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.3%; Scur.
86.4%; Pred. No. 4...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.2%; Scor.
100.0%; Pred. No. o...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSY392_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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NUCLEOTIDE SEQUENCE.
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PROPEP
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                                                                                                                                                                                                                                                         GHRL_CAPHI
                        Matches
                                                                                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                       HIDDEN STATES STATES OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
"cDNA cloning of feline and caprine ghrelin.";
"cDNA cloning of feline and caprine ghrelin.";
Submitted (JUL-2002) to the EMBL/GenBank/DDDA databases.
-!- FUNCTION: Ghrelin is a specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Removed in mature form (By similarity).
/FTId=PRO_000019201.
Obestatin (By similarity).
/FTId=PRO_0000045138.
Removed in mature form (By similarity).
/FTId=PRO_000045139.
Leucine amide (G-99 provides amide group)
                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                          Appetite-regulating hormone precursor (Growth hormone secretagogue)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Amidation of Leu-98 is essential for obestatin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purity Control of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It has an appetite-reducing effect, results in decreased for intake, and reduces gastric emptying activites and jejunal motility (By similarity).
SUBCELLULAR LOCATION: Secreted protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-octanoyl serine (By similarity). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hormone; Lipoprotein; Signal
                                                                                                                                                                     (Growth hormone-releasing peptide) (Motilin-related peptide) (Contains: Ghrelin; Obestatin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8235A51447FFF530 CRC64;
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/FIId=PRO 0000019200.
                  QGBEG6; QGBEG5;
27-SEP-2004, integrated into UniProtKB/Swiss-Prot.
13-SEP-2004, sequence version 1.
07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity)
117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AB089201; BAD34670.1; -; mRNA.
EMBL, AB089202; BAD34671.1; -; mRNA.
InterPro: IPR006737; motilin_assoc.
InterPro: IPR006738; motilin_assoc.
InterPro: IPR006738; motilin_dhrelin.
PANTHER; PTHR112; Preproghrelin; 1.
Pfam; PF04644; Motilin_assoc; 1.
Pfam; PF04644; Motilin_assoc; 1.
Pfam; PR04644; Motilin_assoc; 1.
ProDom; PR0782; Preproghrelin; 1.
ProDom; PD33162; Preproghrelin; 1.
Alternative splicing; Amidation; Hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12956 MW;
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Stomach
                                                                                                                                                                                                                                                                                                                                             Feli
                                                                                                                                                                                                                              Name=GHRL;
FELCA
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                 Felinae;
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Distributed under the Creative Commons Attribution-NoDerivs License
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Leucine amide (G-98 provides amide group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
secretagogue receptor type 1 (GHSR) inducing the release of growth
hormone from the pituitary. Has an appetite-stimulating effect,
induces adiposity and stimulates gastric acid secretion. Involved
in growth regulation (By similarity).
-!- FUNCTION: Obsetatin is a specific ligand for the GPR39 receptor.
It has an appetite-reducing effect, results in decreased food
intake, and reduces gastric emptying activites and jejunal
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penoved in mature form (By similarity).
/FTIG=PRO 0000019199.
/FTIG=RO 0000045136.
/FTIG=RO 0000045136.
Removed in mature form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: Amidation of Leu-97 is essential for obestatin activity (By similarity).
-!- SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) [Contains: Ghrelin; Obestatin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            motility (By similarity).
-!- SUBCELLULAR LOCATION: Secreted protein.
-!- PTM: O-n-octanoylation is essential for ghrelin activity similarity).
  Length 117;
                                                   Indels
                                                                                                                                                             1 MPSPGTVCSLLLFSMLWADLAMAGSSFLSPEHOKVQORKESKKP 44
                                                                                                          1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
Ghrelin (By similarity).
/FTId=PRO_0000019198.
                                                                                                                                                                                                                                                                                                                                                     27-SEP-2004, integrated into UniProtKB/Swiss-Prot. 13-SEP-2004, sequence version 1. 07-FEB-2006, entry version 16.
Score 180; DB 1; I
Pred. No. 1.3e-10;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (By similarity)
                                                                                                                                                                                                                                                                                                    116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom, PD332162, Preproghrelin, 1.
Amidation, Hormone, Lipoprotein, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB089200; BAD34669.1; -; mRNA. InterPro; IPR006737; motilin assoc. InterPro; IPR006734; motilin ghrelin. InterPro; IPR00541; Preproghrelin. PANTHER; PTR14122; Preproghrelin. Pfam; PP04643; Motilin assoc; 1. Pfam; PP04644; Motilin ghrelin; 1.
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pecora; Bovidae; Caprinae; Capra.
29.0%;
79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA]
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01624; GHRELIN
                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capra hircus (Goat).
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Stomach;
                                                   35;
                                                                                                                                                                                                                                                                                                 GHRL CAPHI
Q6BEG7;
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Query Match
Best Local S
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RADGEOLE TO THE CALL TO THE CALL THE C., KOGZIUS R., Shimokawa K., RADGEOLE TO, W., WILLIAM R., RADGEOLE T., LEADARD S., GOUGH J. E., SANDORN, M., MINING L.G., Addinis V., Allen J.E.,

RADGEOLE IMPIONDATO A., Appeller R., AUTHOLIJYA R.N., BRISH Y.L.,

RADGEOLE TO THE CALL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             Eukaryota; Metazia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.
                    Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) (M46 protein) [Contains: Ghrelin; Obestatin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Konno H., Nakano K., Ninomiya
.bata K., Shiraki T., Suzuki S.
                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE 24-30, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                 MEDLINE=20389976; PubMed=10930375; Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; Identification and characterization of a novel gastric peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mouse mRNA for preproghrelin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                              hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
                                                                                          Name=Ghrl; Synonyms=Mtlrp;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                             TISSUE=Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kojima M.
                                                                   protein)
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                                                                                                                                          1 MPSPGTVCSLLLLGMLMLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQL-CDL 59
                                                                                                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              င္ဖ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Gerbillinae, Meriones.
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
PubMed=14724148; DOI=10.1136/gut.2003.021568;
Suzuki H., Masaoka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kangawa K., Ishii H.; "Helicobacter pylori infection modifies gastric and plasma ghrelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
GO; GO:0050791; P:regulation of physiological process; IEA.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR00541; Preproghrelin.
                                                                                          6
                                             Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghrelin preproprotein.
Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWLHPDGRGQAEGAEDELEIRFNAPFDVGIKLSGAQYQQHGRALG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Indels
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QORH-------LWASVFSQSTKDSGSDLTVSGRTWG
CDA67971D72E3303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27657687FC026A74 CRC64;
                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHRL MOUSE STANDARD; PRT; 117 AA. Q9EQXO; Q9WUZ1; 117 AA. 13-DEC-2001, integrated into UniProtKB/Swiss-Prot. 01-MAR-2001, sequence version 1.
                                          27.7%; Score 171.5; DB 1;
42.9%; Pred. No. 1e-09;
ive 13; Mismatches 34;
                                                                                                                                                                                                                                                                     60 EQQRH-----LWASVFSQSTKDSGSDLTVSGRTWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.6%; Score 165; DB 2; 41.0%; Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                            117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF442491; AAO06965.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF04644; Motilin ghrelin; 1. PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PD332162; Preproghrelin;
CE 117 AA; 13035 MW; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dynamics in Mongolian gerbils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04643; Motilin assoc; 1
  12935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                          Query Match
Best Local Similarity 42.9%;
Matches 42; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.6
Best Local Similarity 41.0
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gut 53:187-194(2004).
  116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10047;
                                                                                                                                                                                                                                                                                                                                                                                                            Q8CH53_MERUN
Q8CH53;
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Name=1; Synonym==Ghrelin;
Name=1; Synonym==Ghrelin;
Isoid=OBEXX0-1; Sequence=Displayed;
Name=2; Synonym==d-Gln14-ohrelin;
Isoid=OBEXX0-1; Sequence=Usp.003246;
-: TisSUB SPECIFICITY: Mainly expressed in the gastrointestinal tract with higher levels in the stomach, medium levels in the duodenum, jejunum, ileum and colon. Low expression in the testis and brain.
Not detected in the salivary gland, pancreas, liver and lung.
-:- DEVELOPMENTAL STAGE: Levels of n-otenoylated and n-decanoylated ghrelin drop by one third and 3-fold, respectively, between postnatal weeks 3 and 4 due to change of diet during weaning.
-:- PTW: On-octanoylation is essential for ghrelin activity (By similarity). The O-n-decanoylated form ghrelin-Cl0 differs in the length of the carbon backbone of the carboxylic acid bound to Ser-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                        hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Ghrelin is a specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved
                                                                                                                                                                                                                                                                       MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3; Kojima M., Hosoda H., Matsuo H., Kangawa K.; "Ghrelin: discovery of the natural endogenous ligand for the growth
DEVELOPMENTAL STAGE, AND ACYLATION OF SER-26. PubMed=15746259; DOI=10.1210/en.2004-0645; Nishi Y., Hiejima H., Mifune H., Sato T., Kangawa K., Kojima M.; "Developmental changes in the pattern of ghrelin's acyl modification and the levels of acyl-acolified ghrelins in murine stomach."; Endocrinology 146:2709-2715(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in growth regulation. FUNCTION: Obsertatin is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: Amidation of Leu-98 is essential for obestatin activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom, PD332162; Preproghralin, 1.
Alternative splicing, Amidation, Direct protein sequencing; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=PRO_0000019205.
Removed in mature form (By similarity).
/FTId=PRO_0000019206.
Obestatin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005179; F:hormone activity; TAS.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
PANTHER; PTH814122; Preproghrelin; I.
Pfam; PF04643; Motilin_assoc; I.
Pfam; PF04644; Motilin_assoc; I.
PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motility (By similarity).
SUBCELLULAR LOCATION: Secreted protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB060078; BAB69857.1; -; Genomic_DNA
AK008658; BAB25814.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSMUSG0000064177; Mus musculus. MGI; MGI:1930008; Ghrl. GO; GO:0005737; C:cytoplasm; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghrelin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB035701; BAB19046.1; -; mRNA.
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SIGNAL
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EMBL;
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PubMed=15471962; DOI=10.1210/en.2003-1466;
PubMed=15471962; DOI=10.1210/en.2003-1466;
PubMed=15471962; DOI=10.1210/en.2003-1466;
Herington A.C., Chopin L.K.,
"Expression of the ghrelin axis in the mouse: an exon 4-deleted mouse proghrelin variant encodes a novel C terminal peptide.";
Endocrinology 146:432-440(2005).
                                                                                Leucine amide (G-99 provides amide group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nus.
Bukanyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
/FTIG=PRO 0000045142.
Removed in mature form (By similarity).
/FTIG=PRO_0000045143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                           ghrelin).
O-octanoyl serine (in form n-octanoyl ghrelin) (in isoform 2).
Missing (in isoform 2).
                                                                                                          (By similarity).
O-decanoyl serine (in form n-decanoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AY179430; AA027350.1; -; mRNA.
Ensembl; ENSMUSG0000064177; Mus musculus.
MGI: MGI:1930009; Ghrl.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:016608; P:growth hormone-releasing hormone activity; RCA.
InterPro; IPR006738; motilin ghrelin.
InterPro; IPR00541; Preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                    Score 163; DB 1; Length 117;
Pred. No. 7.9e-09;
7; Mismatches 33; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 162; DB 2; Length 86;
Pred. No. 6.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 GWLHPEDRGQAEETEEELEIRFNAPFDVGIKLSGAQYQQHGRALG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QQRH------LWASVFSQSTKDSGSDLTVSGRTWG
                                                                                                                                                                                                                                                                                             117 AA; 13207 MW; EACB49DZE3CA7203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9758 MW; B913858874770512 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                            003246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                               /FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANTHER, PTRI14122; Preprediction, 1. Pfam; PF04644; Motilin ghrelin, 1. PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2006, entry version 15.
Exon 4-deleted preproghrelin variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                          26.3%;
41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity 70.5
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                86
                                                                                                                                                                                        26
                                                                                                                                                                                                                                            37
                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                        26
                            66
                                                                                86
                                                                                                                                       56
                                                                                                                                                                                                                                               37
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Q811T4;
                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Ghrl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                MOD RES
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                            PROPEP
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  SHARAFA
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- FUNCTION: Girelin is a specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).

--- FUNCTION: Obsertation is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal motility (By similarity).

--- SUBCELLULAR LOCATION: Secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD332162; Preproghrelin; 1.
Alternative splicing, Amidation; Hormone; Lipoprotein; Signal.
SIGNAL 1 23 By similarity.
PEPTIDE 24 51 Ghrelin (By similarity).
//FTId=PRO 0000019196.
PROPEP 52 75 Removed in mature form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9BEF8-2; Sequence=VSP_003244;
-!- PTM: On-octanoylation is essential for ghrelin activity (By similarity).
-!- PTM: Amidation of Leu-98 is essential for obestatin activity (By
                GHRL CANFA STANDARD; PRT; 117 AA.

Q9BEF9; Q9BEF7;

13-DEC-2001, integrated into UniProtKB/Swiss-Prot.

01-UUN-2001, sequence version 1.

07-FEB-2006, entry version 29.

Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-regleasing peptide) (Motilin-related peptide)

(Growth Synonyms=MILRP;

Name=GHRL; Synonyms=MILRP;

Canis familiaris (Dog).
                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [WRNA] (ISOFORMS 1 AND 2).

TISSUE=Gastric fundus;

Tomasetto C., Wendling C., Rio M.-C., Poitras P.;

"Identification of cDNA encoding MTLRE/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
"Dog ghrelin.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AJ298295, CAC29155.1; -; mRNA.
EMBL, AJ298296; CAC29156.1; -; mRNA.
EMBL, AJ298296; CAC29156.1; -; mRNA.
EMBL, AB060700; BAC75929.1; -; mRNA.
InterPro, IPR006737; motilin_assoc.
InterPro, IPR006737; motilin_assoc.
InterPro, IPR006731; motilin_dhtalin.
PANTHER; PTHR14122; Preproghtalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SIMILARITY: Belongs to the motilin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1; Synonyms=Ghrelin;
Isold=Q9BER8-1; Sequence=Displayed;
Name=2; Synonyms=Gel-Gln14-ghrelin;
Isold=Q9BER9-2; Sequence=VSP_003244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF0464; Motilin_ghrelin; 1. PRINTS; PR01624; GHRELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04643; Motilin_assoc; 1.
Pfam; PF04644; Motilin_ghrelin; 1
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Stomach;
GHRL CANFA
```

	FT	PEPTIDE	94	86	/FTIG=Pl	/FTId=PRO_0000019197. Obestatin_(By similarity)	197. Llarity).		
		PROPEP	66	117	Removed /FTIdapi	in mature	0000045134.   mature form (By Bir   0000045135	similarity).	
	: : :	MOD_RES	86	86	Leucine (Bv sim	amide (G-	vides	amide group)	
	F F F	LIPID VARSPLIC	26 37	26 37	O-octanoyl Missing (ir	oyl serine (By s (in isoform 2).	(By similarity) rm 2).	ity).	7
	SO	SEQUENCE	117 AA;	13007 MW;	7 F 1 1 G = V	11G=VSF_003244.	, CRC64;		
	S B E	Query Match Best Local Sim Matches 31;	Similarity 70.	46 46 (	Score 162; Pred. No. 1 5; Mismatch	DB 1; .e-08; tes	Length 117; 8; Indels	; 0; Gaps	0
	ઠે	I MP	SPGTVCSI	MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP	AMAGSSFI	SPEHORVOVI	RPPHKAP 44		
	g	M M	SLGTMCSL		AMAGSSFI	SPEHOKLOQI	KESKKP 44		
	RESULT Q7TSD1 ID	LT 11 D1 MOUSE O7TSD1 MOUS		PRELIMINARY:	PRT:	78 AA.			
	PA PA	Q7TSD1; 01-OCT-2003,	, integr	integrated into UniProtKB/TrEMBL	UniProt	CB/TrEMBL.			
	558	01-OCT-2003 07-FEB-2006	, sequer	sequence version entry version 11.	 				
	3 8 8	Gnrein deitaz. Name=Ghrl; Synonyms=Ghrelin; Mus musculus (Mouse)	Synonyms	=Ghrelin;					
	888	Eukaryota; Mammalia: E	Metazoa; Sutheria:	Chordata; Evarchont	Craniat	a, Verteb	Chordata, Craniata, Vertebrata, Euteleostomi, Euarchontoglires: Glires: Rodentia: Sciurognathi	ostomi; iurognathi;	
	88	Muroidea; Muridae; Murinae; Mus NCBI TaxID=10090;	uridae; 10090;	Murinae; N	fus.				
	R R	[1] NUCLEOTIDE	SEQUENCE	.;	;	:	;		
	\$ <del>1</del> 5	atom nitt	, Nagao JUN-2003	K., Hirate ) to the E	H., Kav MBL/Geni	vano K., H. Sank/DDBJ o			
	មួន	Copyrighted by the Uniprot Consortium, Distributed under the Creative Commons	by the	y the Uniprot Consortium, see http://www.under the Creative Commons Attribution-Nobe	nsortiur re Common	n, see htty ns Attribu	://www.unip	see http://www.uniprot.org/terms Attribution-NoDerivs License	8
	ខ្លួ	EMBL; AB111	891; BAC	AC77409.1; -;	., mRNA.				!
	88	Ensembl; EN MGI; MGI:19	SMUSG000 30008; G	000064177; Shrl.	Mus musc	culus.			
	R R R	GO; GO: 0005 GO; GO: 0005	737; C:c 615; C:e	ytoplasm; extracellul	IDA. ar space	B; RCA.			
	8 B	GO, GO:0016 InterPro; I	608; F:9 PR006737	growth horm '; motilin_	one-rele assoc.	easing horn	one activity	y; RCA.	
	2 K	InterPro; I PANTHER; PT	PR005441 HR14122;	., Preprogh	relin.		InterPro, IPR005441; Preproghrelin. PANTHER; PTHR14122; Preproghrelin; 1.		
	8 8 8 8 8	Pram; Pr04643; MOC11III a PRINTS; PR01624; GHRELIN ProDom; PD332162; Prepro SEOIFENCE 78 AA: 8615	43; MOC1 1624; GH 32162; F 78 AA:	GHRELIN assoc; 1. GHRELIN, Preproghrelin; R615 MW: AD8	in; 1.	1. in; 1. ADB7CB53C9A22FFB CRC64:	RC64 :		
	ಕ	ery Match		6 %;	Score 15	Score 158.5; DB 2	2; Length 78	8;	
	Be	Best Local Sim Matches 37;	Similarity 37; Conserv	ilarity 40.7%; Conservative 11	Pred. No 11; Misma	d. No. 1.4e-08 Mismatches 18		25; Gaps	ä,
	ò	1 MP	SPGTVCSL	LLLGMLWLDI	AMAGSSFI	SPEHORVOVI	MPSPGTVCSLLLLGMLMLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE	LPLSNOLCDLE	09
	g	1 ML	SSGTICSI		AMAGSSFI	SPEHOKAQFI	  APE	FDVGIKLSGAQ	51
	ò	61 00	оокн	LWASI	-LWASVFSQSTKDSGSD	3GSD 80			
, ·	g	52 YQ	:   QHGRALGK	i   YQQHGRALGKFLQDILWEEV					
	RESU GHRL ID	RESULT 12 GHRL RAT ID GHRL RAT	STAN	STANDARD;	PRT;	117 AA.			

ω

Event=Alternative splicing; Named isoforms=2;

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NUCLEOTIDE SEQUENCE (MRNA) (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
STRAIN-Sprager-Daviey, TISSUE-Stomach, MRDLINE-20357315; Pubmed=10801861; DOI=10.1074/jbc.M002784200; Hosoda H., Kojima M., Matsuo H., Kangawa K.; Andrews M., Matsuo H., Mats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ō
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norveyrus (Rat).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Obestatin, a peptide encoded by the ghrelin gene, opposes ghrelin's effects on food intake.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                   Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) [Contains: Ghrelin; Obestatin-23; Obestatin-13].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 76-95, FUNCTION OF OBESTATIN, CHARACTERIZATION, AMIDATION, MASS SPECTROMETRY, AND INTERACTION WITH GPR39. PubMed=16284174; DOI=10.1126/science.1117255; Zhang J.V., Ren P.G., Avsian-Kretchmer O., Luo C.W., Rauch R., Klein C., Hsueh A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), PROTEIN SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
STRAIN-Sprague-Dawley; TISSUE-Stomach;
MEDLINE-20067959; Pubmed-10604470; DOI-10.1038/45230;
Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553; Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y., Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.; "Structure-activity relationship of ghrelin: pharmacological study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
13-DEC-2001, integrated into UniProtKB/Swiss-Prot. 01-MAY-2000, sequence version 1. 07-MAR-2006, entry version 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in gastrointestinal tissue.";
Biochem. Biophys. Res. Commun. 279:909-913(2000)
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Biochem. Biophys. Res. Commun. 287:142-146(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE-ACTIVITY RELATIONSHIP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        effects on food intake.";
Science 310:996-999(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21092536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                       Name=Ghrl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVIEW
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GO; GO:0005615; C:extracellular space; IC.
GO; GO:0005615; C:extracellular space; IC.
GO; GO:0001664; F:G-protein-coupled receptor binding; IPI.
GO; GO:00016608; F:growth hormone-releasing hormone activity; IDA.
GO; GO:0007186; P:growth hormone-releasing hormone activity; IDA.
GO; GO:000718; P:growth hormone-releasing hormone activity; IDA.
GO; GO:0050791; P:regulation of physiological process; NAS.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
PANTHER; PTHR14122; Preproghrelin, 1.
Pfam; PF04643; Motilin_ghrelin; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
PFRNIS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
            Name=1; Synonyms=Ghrelin; Isode-Displayed; Isode-OgOYH7-1; Sequence-Displayed; Name=2; Synonyms=del-Gln14-ghrelin; IsoId=OgOYH7-2; Sequence=VSP_003248; IsoId=OgOYH7-2; Sequence=VSP_003248; IsoId=OgOYH7-2; Sequence=VSP_003248; expressed with higher expression in the stomach. Very low levels are detected in the hypothalamus, heart, lung, pancreas, intestine and adipose tissue. Obstatin is most highly expressed in jejunum, and also found in duodenum, stomach, pituitary, ileum, liver, hypothalamus and heart. Expressed in low levels in pancreas, cerebellum, cerebrum,
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the motilin family.
DATABASE: NAME=Protein Spotlight; NOTE=Issue 66 of January 2006;
WWW="http://www.expasy.org/spotlight/back_issues/sptlt066.shtml".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD332162; Preproghrelin; 1.
Alternative splicing; Amidation; Direct protein sequencing; Hormone;
                                                                                                                                                                                  kidney, testis, ovary colon and lung.
PTM: O-n-octanoylation is essential for ghrelin activity. The
replacement of Ser-26 by aromatic tryptophan preserves ghrelin
                                                                                                                                                                                                                                                  -!- PTM: Amidation of Leu-98 is essential for obestatin activity.
-!- MASS SPECTROMETRY: MW=3314.9; MW ERR=0.7; METHOD=Electrospray;
RANGE=24-51 (090YH7-1); NOTE=Ref.1.
-!- MASS SPECTROMETRY: MW=3187.1; MW ERR=0.6; METHOD=Electrospray;
RANGE=24-50 (090YH7-2); NOTE=Ref.2.
-!- MASS SPECTROMETRY: MW=2516.3; METHOD=UNKnown; RANGE=76-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTIG=PRO 0000045148.
Leucine amide (G-99 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 158; DB 1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8857546FE51A7691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=PRO 0000045146.
Obestatin-13 (Probable)
/FTId=PRO 0000045147.
Removed in mature form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=PRO 0000019209.
Removed in mature form.
/FTId=PRO 0000019210.
Obestatin-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSRNOG0000010349; Rattus norvegicus. RGD; 632283; Ghrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB029433; BAA89370.1; -; mRNA.
EMBL; AB035699; BAB11956.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA; 13176 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 40.0
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
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37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; B59316; B59316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                        activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
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9 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLE

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SUBCELLÚLAR LOCATION: Secreted protein. ALTERNATIVE PRODUCTS:

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7; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                 Baviskar P.S., Mitra A.; 
Tharacterization of ghrelin gene of zebu cattle (Bos indicus) and 
"faaloes (Bubalus bubalis)."; 
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
07-FEB-2006, entry version 2.
Ghrelin precursor (Fragment).
Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bubalus.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL, DQ118139; AAZ38152.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
GO; GO:0050791; P:regulation of physiological process; IEA.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04644; Moctilin ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY373019; AAR24571.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity;
GO; GO:0050791; P:regulation of physiological process; IEA.
InterPro; IPR005738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
PANTHER; PTHR14122; Preproghrelin; 1.
PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.7%; Score 153; DB 2; Length 49; 69.0%; Pred. No. 3.1e-08; ive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Pig Ghrelin.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AA; 7980 MW; 875424C2D41FC166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6ABB94634997FAC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPAPWTICSLLLLSVLCMDLAWAGSSFLSPEHQKLQRKEPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2004, sequence version 1. 07-FBB-2006, entry version 6. Ghrelin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rothschild M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similari, nes 29; Conservative
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49
49
49
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig)
                                                                                                                                                                                                                TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q67BBS PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SIGNAL
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Q67BB5_
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                            1 MVSSATICSLLLLSMLWMDMAMAGSSFLSPEHQKAQQRKESKKP-----PAKLQPRALE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPAPRIIYSLLLLSLLWMDLAMAGSSFLSPEHQKLQRKEPKKPSGRLKPRALEGQFDPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQL-CDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
GO; GO:0016609; F:growth hormone-releasing hormone activity; IEA.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
PANTHER; PTHR14122; Preproghrelin.
PERM: PP04644; Motilin_assoc; 1.
PERM: PP04644; Motilin_assoc; 1.
PERM: PP04644; Motilin_assoc; 1.
PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                             Preproghrein precursor.
Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Stomach;
Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa
"sheep ghrelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lv D.Y., Cao G.F., Bai C.L., Xu R.G.;
"Mongolia sheep ghrelin mRNA.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                             50 ghrelin.
12977 MW; B78ECA3DBF0E568E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 EQQRH-----LWASVFSQSTKDSGSDLTVSGRTWG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSÓEEGAEDELEIRFNAPFNIGIKLSGAQSLQHGQTLG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.4%; Score 157.5; DB 2
Best Local Similarity 40.8%; Pred. No. 2.9e-08;
Matches 40; Conservative 14; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
Q45RQ6 BUBBU

Q45RQ6 BUBBU

AC Q45RQ6;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
                                                                                                                                                                                                                                                  01-JUN-2003, integrated into UniProtKB/TrEMBL, 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 12.
                                                                                                                                                                                                              116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB060699; BAC75928.1; -; mRNA.
EMBL; DQ294307; ABC00742.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01624; GHREL<u>I</u>N.
ProDom; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
24
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Stomach;
                                                                                                                                                                                                              Q863L0 SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SOTT WAR BRANK BRA

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Query Match 24.3%; Score 150.5; DB 2; Length 74; Best Local Similarity 71.1%; Pred. No. 9.1e-08; Matches 32; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Search completed: July 11, 2006, 17:05:19 Job time : 298 secs

174 Wall

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Query Match 31.9%; Score 198; DB 2; Length 117; Best Local Similarity 88.6%; Pred. No. 4.4e-17; Matches 39; Conservative 0; Mismatches 5; Indels
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FRAGMENT TYPE:
US-09-046-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ropology:
                                                                                                                                                                                                                                                                                                                                               US-09-046-479-2
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                                                                               July 11, 2006, 17:05:38; Search time 50 Seconds (without alignments) 204.822 Million cell updates/sec
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                                                                                                                                                                    1 MPSPGTVCSLLLLGMLWLDL.......PPSSRERSRRSHQPSCSPEL 117
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Sequence 2,
Sequence 2,
Sequence 2,
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: / EMC Celerra SIDS3/ptodata/2/laa/5_COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/laa/6_COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/laa/7_COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/laa/H_COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/laa/FCTUS_COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/laa/FCTUS_COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/laa/RE_COMB.pep:*
: / EMC Celerra_SIDS3/ptodata/2/laa/RE_COMB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-997-349-268
US-09-997-653-268
US-09-989-293A-268
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US-09-997-333-268
US-09-992-598-268
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US-09-989-726-268
US-09-997-514-268
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US-09-853-253-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Perfect score:
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US-10-276-392-10 US-10-276-392-11 US-10-276-392-13 US-10-276-392-14 US-10-276-392-14 US-10-276-392-16 US-10-276-392-17 US-10-276-392-17 US-10-276-392-19 US-10-276-392-19 US-10-276-392-19 US-10-276-392-19 US-10-276-392-19 US-09-252-991A-27248 US-09-252-991A-27248 US-09-949-016-7800 US-09-949-016-7800 US-09-949-016-7801 US-09-949-016-7801 US-09-949-016-7801	99
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## ALIGNMENTS

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SOFTWARE: DOS
SOFTWARE: PSELSED for Windows Version 2.0
SOFTWARE: PSELSED for Windows Version 2.0
CURRENT APPLICATION DATA:
PRILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak
Sequence 2, Application US/09046479
Patent No. 6291653
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                            ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Savislak, Deborah A
REGISTRATION NUMBER: 37,438
REFRENCE/DOCKET NUMBER: 97-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                       COUNTR:
2IP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
""""TER: DISKETTE
"""" DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 117 amino acid TYPE: amino acid
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internal
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STATE: WA
COUNTRY: USA
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Species existence of

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88.6%; Pred. No. 4.4e-17;
tive 0; Mismatches 5; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERG for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%; Score 198; DB 2;
88.6%; Pred. No. 4.4e-17;
ative 0; Mismatches 5.
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US-09-794-987-2
Sequence 2, Application US/09794987
Sequence 6.838438
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Bleppard, Paul O.
APPLICANT: Deisher, Theresa A.
APPLICANT: Daspers, Stephen R.
FILE REFERENCE: 97-04CI
CURRENT APPLICATION NUMBER: US/09/404,417A
CURRENT APPLICATION NUMBER: US/09/404,417A
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
SEQ IF NO 2
TYPE: PRT
CURRENT FILING DATE: 2000-06-30
PRICR APPLICATION NUMBER: 60/141,592
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 117
TYPE: PRT
CORANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09404417A; Patent No. 6627729; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98102
COMPUTER READABLE FORM:
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Best Local Similarity 88.6'
                                                                                                                                                                                                                                                                                                                                                     39; Conservative
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                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                     ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
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US-09-404-417A-2
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31.9%; Score 198; DB 2; Length 11
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels
                                                    1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                           1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98102
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09608810A
Patent No. 6420521
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Daspers, Stephen R.
APPLICANT: Daspers, Stephen R.
APPLICANT: Bishop, Paul D.
TITLE COF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
                                                                                                                                                                   Sequence 2, Application US/08822897C
Patent No. 63801S8
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOWOLOGS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislar, Deborah A
REGISTRATION NUMBER: 97-04
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                     STREET: 1201 Eastlake Avenue CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                      US-08-822-897C-2
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APPLICANT: Shord, ALLILAM 1.

APPLICANT: Shord, ALLILAM 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION WINER: 60/6250 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION WINER: 60/6311 PRIOR APPLICATION WINER: 60/6312 PRIOR APPLICATION WINER: 60/6302 PRIOR APPLICATION WINER: 60/6303 PRIOR APPLICATION WINER: 60/63
                                                                                                                                                                                                                                                                    Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                       Ferrara, Napoleone
Fong, Sherman
                                                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                        Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                         Kljavin, Ivar J.
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                                                     Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                           Godowski, Paul
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APPLICANT:
APPLICANT:
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31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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31.9%; Score 198; DB 2;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5.
                   PRIOR DATE: 27-Eb-2001
CLASIPICATION: GUNDOWN:
PRIOR APPLICATION: GUNDOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: GUNDOWN:
ATTORNEY, AGENT INFORMATION:
NAME: Sawielak, Deborah A
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 37,438
REGISTRANCE, DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAK: 206-442-6678
TELEFAK: CUNROWN:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squence 2, Application US/09853253
Fatent No. 6897286
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: JASPERS, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR PRILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTHARR: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                           | LENGTH: 117 anino acids | TENGTH: amino acids | TOPOLOGY: 1inear | MOLECULE TYPE: procein | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-794-987-2
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; Sequence 268, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-853-253-2
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Gaps .. 0 Length 117; 31.9%; Score 198; DB 2; Length 11 88.6%; Pred. No. 4.4e-17; ive 0; Mismatches 5; Indels 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR PAPLICATION NUMBER: 60/090445
PRIOR PLING DATE: 1938-06-24
PRIOR PLING DATE: 1938-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR PELING DATE: 1938-06-24
PRIOR PELING DATE: 1938-06-25
PRIOR PELING DATE: 1938-06-25
PRIOR PELING DATE: 1938-06-25
PRIOR PELING DATE: 1938-06-25
PRIOR PAPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1938-06-25
PRIOR PELING DATE: 1938-06-26
PRIOR PELING DATE: 1938-07-01
PRIOR PELING DATE: 1938-07-01
PRIOR PELING DATE: 1938-07-02
PRIOR PELING DATE: 1938-07-03
PRIOR PELING DATE: 1938-07-03
PRIOR PELING DATE: 1938-07-07
PRIOR PELING D Sequence 268, Application US/09990444 Patent No. 6930170 GENERAL INFORMATION: Eaton, Dan L. Ferrara, Napoleone Fong, Sherman Gerber, Hanspeter APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David 39; Conservative Desnoyers, Luc Query Match Best Local Similarity US-09-990-444-268 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Matches ઠે g

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PRIOR APPLICATION NUMBER: 60/08655
PRIOR FILING DATE: 1998-06-09
PRIOR PILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08812
PRIOR PLILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR PLILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-23
PRIOR PLILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF STATE AND SECRET AND 
                                                                Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
                                                                                                                                                                                                                                                                                             Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
         Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C27
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FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%; Score 198; DB 2;
88.6%; Pred. No. 4.4e-17;
iive 0; Mismatches 5;
                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/796,158
FILING DATE: 28-Feb-2001
CLASSIFICATION AUMBER: US/09/796,158
FILING DATE: 28-Feb-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA: 09/046,479
FILING DATE: cURKNOWN>
ATORNEY/AGENT INFORMATION:
NUMBER: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 37,438
TELEFRAN: 206-442-6673
TELEFRAN: 206-442-6673
TELEFRAN: 206-442-6673
TELEFRAN: CURROWN>
TELEFRON: 106-073
TELEFRON: 106-073
TELEFRON: 206-442-6678
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CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 268, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
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PRIOR APPLICATION UNDBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
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Gerber, Hanspeter
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Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker,Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski, Paul
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Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-997-333-268
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STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
APPLICATION NUMBER: 60/090695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
                                                                                                                                                                                                    FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090678
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091544
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APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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                                                                                                                                                                       APPLICATION NUMBER: 60/090542
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Patent No. 6939690
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.9%;
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FILING DATE: 1998-06-24
                                                                                                                                    FILING DATE: 1998-06-24
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Best Local Similarity 88.6
Matches 39; Conservative
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PRIOR PLINED APPLICATION WURBER: 60,065186
PRIOR TILING DATE: 1997-11.12
PRIOR PLINED APPLICATION WURBER: 60,065311
PRIOR PLINED APPLICATION WURBER: 60,066770
PRIOR PLINED APPLICATION WURBER: 60,06771
PRIOR PLINED APPLICATION WURBER: 60,075945
PRIOR PLINED APPLICATION WURBER: 60,078916
PRIOR PLINED APPLICATION WURBER: 60,078916
PRIOR PLINED APPLICATION WURBER: 60,081302
PRIOR PLINED APPLICATION WURBER: 60,081302
PRIOR PLINED APPLICATION WURBER: 60,08106
PRIOR PLINED APPLICATION WURBER: 60,08106
PRIOR PRIOR PLINED APPLICATION WURBER: 60,08107
PRIOR PLINED APPLICATION WURBER: 60,08107
PRIOR PRIOR PLINED APPLICATION WURBER: 60,08102
PRIOR PRIOR PLINED APPLICATION WURBER: 60,08102
PRIOR PRIOR PLINED APPLICATION WURBER: 60,08103
PRIOR PRIOR PLINED APPRICATION WURBER: 60,08103
PRIOR PLINED APPRICATION WURBER: 60,08103
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PRIOR PLINED APP

R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24 R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
R PAPPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 6//090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 FILING DATE: 1998-06-18 FILING DATE: 1998-06-22 FILING DATE: 1998-06-25 

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APPLICATION NUMBER: 60/089538
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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31.9%; Score 198; DB 2; Length 117;
1 Similarity 88.6%; Pred. No. 4.4e-17;
39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
              A APPLICATION NUMBER: 60/091360
BR FILING DATE: 1998-07-01
BR FILING DATE: 1998-07-02
BR PELING DATE: 1998-07-02
BR APPLICATION NUMBER: 60/091544
BR FILING DATE: 1998-07-01
BR FILING DATE: 1998-07-01
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R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
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R FILING DATE: 1997-11-24
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Patent No. 6956108
GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
Roy, Margaret Ann
  FILING DATE: 1998-06-26
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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Best Local Similarity
Matches 39; Conserva
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US-09-992-598-268
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R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/08332
R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
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R APPLICATION NUMBER: 60/08106
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 66/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 66/088030
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-05
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PRIOR PELICATION UNDERS: 06/09959
PRIOR PELING DATE: 1999-06-17
PRIOR PELING DATE: 1999-06-19
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PRIOR PELICATION UNDERS: 60/09901
PRIOR PELING DATE: 1999-06-19
PRIOR PELICATION UNDERS: 60/09046
PRIOR PELING DATE: 1999-06-22
PRIOR PELICATION UNDERS: 60/09046
PRIOR PELING DATE: 1999-06-22
PRIOR PELICATION UNDERS: 60/09046
PRIOR PELING DATE: 1999-06-22
PRIOR PELICATION UNDERS: 60/09046
PRIOR PELING DATE: 1999-06-23
PRIOR PELICATION UNDERS: 60/09045
PRIOR PELING DATE: 1999-06-24
PRIOR PELING DATE: 1999-06-25
PRIOR PELING DATE: 199
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and Transmembrane Polypeptides and Nucleic Gaps .; 0 1 MPSPGTVCSLLLIGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 31.9%; Score 198; DB 2; 88.6%; Pred. No. 4.4e-17; tive 0; Mismatches 5, APPLICANT: WILLIAMS, FILEARY
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane FITILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC61
CURRENT APPLICATION NUMBER: US/09/089,735
CURRENT FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PLING DATE: 1998-01-25
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075915
PRIOR APPLICATION NUMBER: 60/075916
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-04-28
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PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-28 PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1990-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/09198
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 RESULT 12 10S-05-989-735-268 : Sequence 268, Application US/09989735 ; Patent No. 6972185 Grimaldi, J. Christopher Gurney, Austin L. Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Ferrara, Napoleone Fong, Sherman Paoni, Nicholas F. Gerber, Hanspeter Gerritsen, Mary E. Query Match Best Local Similarity 88.6 Matches 39; Conservative Kljavin, Ivar J. Napier, Mary A. APPLICANT: Ashkenazi, Avi J. Baker, Kevin P. Botstein, David Goddard, Audrey Godowski, Paul Desnoyers, Luc Eaton, Dan L. Pan, James GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: ద ਨੇ

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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1938-66-18
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PRIOR FILING DATE: 1938-66-19
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PRIOR PRICATION NUMBER: 60/08045
PRIOR PLING DATE: 1938-66-19
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PRIOR PLING DATE: 1938-66-25
PRIOR APPLICATION NUMBER: 60/090659
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PRIOR APPLICATION NUMBER: 60/08759
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
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PRIOR PLILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08025
PRIOR PLILING DATE: 1998-06-04
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APPLICANT: Walliams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
I TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P3730PLCG
CURRENT APPLICATION NUMBER: 05/049787
PRIOR APPLICATION NUMBER: 60/045787
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
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31.9%; Score 198; DB 2; Lo
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5;
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Patent No. 7018811
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
  PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
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Napier, Mary A.
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US-09-989-726-268
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Gaps ;

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Best Local Similarity 88.6%; Pred. No. 4.4e-17; Matches 39; Conservative 0; Mismatches 5;

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A APPLICATION NUMBER: 60/08948

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/08952

R APPLICATION NUMBER: 60/090246

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R APPLICATION NUMBER: 60/090253

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090254

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090359

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090355

R FILING DATE: 1998-06-23

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R APPLICATION NUMBER: 60/090557
R APPLICATION NUMBER: 60/090676
R APPLICATION NUMBER: 60/090678
R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R RAPLICATION NUMBER: 60/091478
R RAPLICATION NUMBER: 60/091478
R RAPLICATION NUMBER: 60/09154
R RELING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-06-26
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
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APPLICATION UNMBER: 60/090431
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090694
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### APPLICANY: Sacreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/997,514

CURRENT PILING DATE: 1997-10-11-5

PRIOR FILING DATE: 1997-10-11-13

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PRIOR FILING DATE: 1997-11-12

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PRIOR PELING DATE: 1998-05-20

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PRIOR PELING DATE: 1998-06-02

PRIOR PELING DATE: 1998-06-02

PRIOR PELING DATE: 1998-06-03

PRIOR PELING DATE: 1998-06-03
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US-09-997-514-268
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; Eatent No. 7019116
; GENERAL INFORMATION:
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Gerber, Hanspeter
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Kljavin, Ivar J.
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PRIOR PILING DATE: 1998-06-04
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PRIOR PAPLICATION NUMBER: 60/08028
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PRIOR PELING DATE: 1998-66-04
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PRIOR PILING DATE: 1998-66-05
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PRIOR PILING DATE: 1998-66-05
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PRIOR PILING DATE: 1998-66-05
PRIOR APPLICATION NUMBER: 60/08021
PRIOR PILING DATE: 1998-66-05
PRIOR PILING DATE: 1998-66-10
PRIOR APPLICATION NUMBER: 60/08956
PRIOR PILING DATE: 1998-66-10
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PRIOR PELLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR PELLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
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PRIOR APPLICATION NUMBER: 60/090445
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09166
PRIOR PELLING DATE: 1998-07-01
PRIOR PELLING DATE: 1998-

Query Match 31.9%; Score 198; DB 3; Length 117;
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Matches 39; Conservative 0; Mismatches 5; Indels 0;
I MPSPGTVCSLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP 44

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APPLICANT: Zhang, Zhang, Zhiniam I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: US/09/989,728

CURRENT PLING DATE: 1997-06-16

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PRIOR FILING DATE: 1997-06-11-12

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PRIOR PELLON NUMBER: 60/08323

PRIOR
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Patent No. 7029873
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APPLICANT: Ashkenazi, Avi J.
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Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timcthy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Goddard, Audrey
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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                              RESULT 15
US-09-989-728-268
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FILING DATE: 1998-06-23

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FILING DATE: 1998-07-09
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Gaps ö Score 198; DB 3; Length 117; Pred. No. 4.4e-17; 0; Mismatches 5; Indels Query Match
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Matches 39; Conservative

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Search completed: July 11, 2006, 17:07:00 Job time : 50 secs

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Query Match
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Matches 116; Conservative
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                                                                July 11, 2006, 17:17:28 ; Search time 176 Seconds (without alignments) 307.933 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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        5.1.9
Biocceleration Ltd.
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US-09-989-723-268
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-09-989-730-268
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Sequence 3, Application US/10294191A

Sequence 3, Application US/10294191A

Publication No. US20030211512A1

GENERAL INFORMATION:
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Publication No. US20050059015A1
GENERAL INFORMATION:
APPLICANT: Mintz, Liat
TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing,
TITLE OF INVENTION: Monitoring and Treating Obesity and/or Diabetes
FILE REFERENCE: 28238
CURRENT PILITING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 42
SOPTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                     US-09-989-724-268
US-09-999-728-268
US-09-993-647-268
US-09-997-428-268
US-09-997-666-268
US-09-990-711-268
US-09-990-711-268
US-09-990-711-268
US-09-991-156-268
US-09-991-157-268
US-09-991-157-268
US-09-991-157-268
US-09-991-1172-268
US-09-997-573-268
US-09-997-573-268
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31.9%; Score 198; DB 3; Length 117;
88.6%; Pred. No. 2.2e-13;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
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Similarity 88.6%; Pred. No. 2.2e-13;
39; Conservative 0; Mismatches 5
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APPLICANT: SHEPPARD, PAUL
APPLICANT: BLEISHEN, THERESA
TITLE OF INVENTION: Zaiga3-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 2
                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37, 438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                               STRANDENNESS: single
TOPOLGGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                           APPLICATION NUMBER: 09/046,479
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 268, Application US/09989722; Patent No. US20020072067A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.; APPLICANT: Baker, Kevin P.; APPLICANT: Besterin, David; APPLICANT: Besterin, David; APPLICANT: Besterin, David; APPLICANT: Beston, David; APPLICANT: Baton, Dan L.
                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.63
Matches 39; Conservative
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Best Local Simil
Matches 39; (
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US-09-989-722-268
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APPLICANT: Chopin, Lisa K

APPLICANT: Deffery, Penelope L

APPLICANT: Jeffery, Penelope L

APPLICANT: Herington, Adrian C

TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
FILE REFERENCE: 225181

CURRENT FILING DATE: 2003-11-10

PRIOR PILING DATE: 2003-11-10

PRIOR PLING DATE: 2001-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10
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                                                                                                     DB 4; Length 60;
                                                                                                  31.9%; Score 198; DB 4; Length 60
88.6%; Pred. No. 1e-13;
.ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVOORKESKKP 44
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: CURRENT APPLICATION: APPLICATION COMPANDED CLASSIFICATION: CURRENT APPLICATION: CURRENT
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Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09794987 Patent No. US20010041791A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/10477506
; Publication No. US20040157227A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 91
                                                                                        Query Match
Best Local Similarity 88.6'
Matches 39; Conservative
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STATE: WA
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ORGANISM: Homo sapiens
US-10-477-506-2
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; TYPE: PRT
; ORGANISM: Human
US-10-294-191A-3
                                                                                                                                                                                                                                                                                                                                             US-10-477-506-2
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US-09-794-987-2
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R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/08655

R FILING DATE: 1998-06-09

R APPLICATION NUMBER: 60/088734

R APPLICATION NUMBER: 60/088738

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088742

R FILING DATE: 1998-06-10

R R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088810

R FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                  R AFFLICATION NUMBER: 60/086858
R APPLICATION NUMBER: 60/086858
R APPLICATION NUMBER: 60/08661
R APPLICATION NUMBER: 60/08861
R APPLICATION NUMBER: 60/08861
R APPLICATION NUMBER: 60/08976
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-16
R FILING DATE: 1998-06-16
R FILING DATE: 1998-06-16
R FILING DATE: 1998-06-16
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FFILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
APPLICATION NUMBER: 60/089599
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/09035
APPLICATION NUMBER: 60/090429
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/088826
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      PRIOR
PRIOR
PRIOR
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APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730PIC63
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/989,722 CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06250
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-0-2-25
PRIOR PELICATION NUMBER: 60/076910
PRIOR PELING DATE: 1998-0-3-20
PRIOR PELING DATE: 1998-0-3-20
PRIOR PELICATION NUMBER: 60/08332
PRIOR PELING DATE: 1998-0-3-20
PRIOR PELING DATE: 1998-0-6-0-3
PRIOR PELING DATE: 1998-0-6-0-3
PRIOR PELING DATE: 1998-0-6-0-4
PRIOR PELING DATE: 1998-0-6-0-6
PRIOR PELING D
                                                                                 Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                     Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
  Ferrara, Napoleone
                                                                                                                                                                                                                                             Roy, Margaret Ann
Stewart, Timothy
Tumas, Daniel
                                          Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                          Paoni, Nicholas F.
                                                                                                                                                             Kljavin, Ivar J
                                                                                                                                                                                Napier, Mary A.
                           Pong, Sherman
                                                                                                                                                                                                       Pan, James
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APPLICANT:
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### PRICANT: Zhang, Zemin | APPLICANT: Zhang, Zemin | APPLICANT: Zhang, Zemin | Title OF INVARITOR: Secreted and Transmembrane Polypeptides and Nucleic | Title OF INVARITOR: Secreted and Transmembrane Polypeptides and Nucleic | Title OF INVARITOR: Secreted and Transmembrane | Polypeptides and Nucleic | Title REFERENCE: 277:091625 | CURRENT FAPLICATION NUMBER: 60/04297 | CURRENT FAPLICATION NUMBER: 60/04297 | CURRENT FILMS DATE: 1997-11-24 | COMPANION: 1998-10-2-2 | PRIOR PELING DATE: 1998-1
                                                                                                 Pan, James Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                  Napier, Mary A.
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                      A APPLICATION NUMBER: 60/09635

B FILING DATE: 1998-06-24

B RILING DATE: 1998-06-24

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B APPLICATION NUMBER: 60/090540

B RILING DATE: 1998-06-24

B RILING DATE: 1998-06-24

CRAPHICATION NUMBER: 60/09057

B FILING DATE: 1998-06-25

CRAPHICATION NUMBER: 60/090676

B RILING DATE: 1998-06-25

CRAPHICATION NUMBER: 60/090690

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CRAPHICATION NUMBER: 60/090690

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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R APPLICATION NUMBER: 60/091544
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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-26
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Grimaldi, J. Christopher
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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Gerber, Hanspeter
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Best Local Similarity
Matches 39; Conserva
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PRIOR APPLICATION NUMBER: 60/08438
PRIOR FILING DATE: 1998-6610
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PRIOR PAPLICATION NUMBER: 60/08916
PRIOR PAPLICATION NUMBER: 60/08926
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PRIOR PAPLICATION NUMBER: 60/08926
PRIOR PAPLICATION NUMBER: 60/08929
PRIOR PRILING DATE: 1998-66-19
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR PRILING DATE: 1998-66-19
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR PRILING DATE: 1998-66-19
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR PRILING DATE: 1998-66-27
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR PRILING DATE: 1998-66-24
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PRIOR PRILING DATE: 1998-66-24
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR PAPLICATION NUMBER: 60/08939
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Gaps . 0 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP Score 198; DB 3; Pred. No. 2.2e-13; 0; Mismatches 5 PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR APPLICATION NUMBER: 60/090542
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
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PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07 Sequence 268, Application US/09989279 Patent No. US20020072496A1 GENERAL INFORMATION: Grimaldi, J. Christopher Gurney, Austin L. 31.9%; 88.6%; Ferrara, Napoleone Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy Gerber, Hanspeter Gerritsen, Mary E Query Match Best Local Similarity 88.6 Matches 39, Conservative APPLICANT: Ashkenazi, Avi J Botstein, David Kljavin, Ivar J Goddard, Audrey Napier, Mary A. Baker, Kevin P. Desnoyers, Luc Eaton, Dan L. Godowski, Paul Fong, Sherman Pan, James APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT g ઠે

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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
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PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-24
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APPLICANT: Tummas, Daniell
APPLICANT: Tummas, Daniell
APPLICANT: Tummas, Daniell
APPLICANT: Wood, Williams Colling
APPLICANT: ADDRESS: Wood, Williams Colling
APPLICANT: ADDRESS: Wood, Williams Colling
TITLE OF INVENTION: Acid Encoding the Same
TITLE OF INVENTION WORDER: GO/G650
PRIOR FILING DATE: 1997-10-76
PRIOR PLING DATE: 1997-10-76
PRIOR PLING DATE: 1997-00-76
PRIOR APPLICATION WORDER: GO/G650
PRIOR APPLICATION WORDER: GO/G850
PRIOR PLING DATE: 1998-60-70
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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CURRENT FILING DATE: 2001-11-19
PRICOR PEDICATION NUMBER: US/09/99,727
CURRENT FILING DATE: 2001-11-19
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PRICOR FILING DATE: 1997-06-16
PRICOR FILING DATE: 1997-06-16
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PRICOR FILING DATE: 1997-11-13
PRICOR FILING DATE: 1997-11-24
PRICOR APPLICATION NUMBER: 60/065311
PRICOR FILING DATE: 1998-0-2-26
PRICOR FILING DATE: 1998-0-2-26
PRICOR PRILOR PAPE: 1997-11-24
PRICOR PRILOR DATE: 1998-0-2-26
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PRICOR PRILING DATE: 1998-0-6-0-3

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Pred. No. 2.2e-13;
0; Mismatches 5
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR APPLICATION NUMBER: 60/090694
PRIOR APPLICATION NUMBER: 60/090694
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR APPLICATION NUMBER: 60/091869
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
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Patent No. US20020072497A1
GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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31.9%;
Best Local Similarity 88.6%;
Matches 39; Conservative
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Gerritsen, Mary E.
Goddard, Audrey
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Eaton, Dan L.
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Grimaldi, J.Ch
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PRIOR APPLICATION NUMBER: 60/08916
PRIOR PILING DATE: 1998-06-11
PRIOR PELICATION NUMBER: 60/08940
PRIOR PELICATION NUMBER: 60/089410
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-24
PRIOR PLI
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FILING DATE: 1998-06-25
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C70 Gaps .; 0 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP Score 198; DB 3; Pred. No. 2.2e-13; 0; Mismatches PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091631
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 Sequence 268, Application US/09989731 Patent No. US20020103125A1 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 Grimaldi,J.Christopher Gurney,Austin L. Kljavin,Ivar J. Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin 31.9%; Eaton, Dan L. Ferrara, Napoleone Gerritsen, Mary E. Gerber, Hanspeter Query Match
Best Local Similarity 88.6°
Matches 39; Conservative GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. Baker, Kevin P. Botstein, David Goddard, Audrey Napier, Mary A. Godowski, Paul Fong, Sherman RESULT 10 US-09-989-731-268 APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/989,731 CURRENT FILING DATE: 2001-11-20

CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-6-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

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PRIOR APPLICATION NUMBER: 60/065186

PRIOR PILICAD DATE: 1997-11.1

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PRIOR PILICATION NUMBER: 60/065111

PRIOR PILICATION NUMBER: 60/07512

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PRIOR PILICATION NUMBER: 60/07759

PRIOR PILICATION NUMBER: 60/08702

PRIOR PILICATION NUMBER: 60/08021

PRIOR PILICATION NUMBER: 60/08032

PRIOR PILICATION NUMBER: 60/08034

PRIOR PILICATION NUMBER: 60/08036

PRIOR PILICATION

PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION UNDER: 60/08534
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-24
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NR APPLICATION NUMBER: 60/078910

R FILING DATE: 1998-03-20

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-28

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/087106

R RILING DATE: 1998-05-28

R FILING DATE: 1998-06-02
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R FILING DATE: 1998-06-10

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R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088858

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088861

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088861

R APPLICATION NUMBER: 60/088861
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R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087827
R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/088021
R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088026
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/088030

R FILING DATE: 1998-06-04

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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088326
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212
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R APPLICATION NUMBER: 60/088738

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R APPLICATION NUMBER: 60/088742

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R APPLICATION NUMBER: 60/08810

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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-02
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APPLICANT: Anny, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C57
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Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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DR APPLICATION NUMBER: 60/091360
DR FILING DATE: 1998-07-01
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DR APPLICATION NUMBER: 60/091478
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091519
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DR APPLICATION NUMBER: 60/091519
DR PILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091636
DR APPLICATION NUMBER: 60/091636
DR APPLICATION NUMBER: 60/09163
DR APPLICATION NUMBER: 60/091978
DR APPLICATION NUMBER: 60/09198
DR APPLICATION NUMBER: 60/09198
DR PILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
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DR APPLICATION NUMBER: 60/09182
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Patent No. US20020123463A1
GENERAL INFORMATION:
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
Tumas, Daniel
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Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
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Napier, Mary A.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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PRIOR APPLICATION NUMBER: 60/08599
PRIOR FILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
PRIOR PAPLICATION NUMBER: 60/08563
PRIOR APPLICATION NUMBER: 60/08961
PRIOR APPLICATION NUMBER: 60/089691
PRIOR APPLICATION NUMBER: 60/08998
PRIOR PILING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-25
PRIOR PELLING DATE: 1998-07-03
PRIOR PELLIN
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT FILING DATE: 2001-111-14

PRIOR PLING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1997-11-24

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR PLING DATE: 1998-04-28

PRIOR PLING DATE: 1998-04-28 Gaps ö Score 198; DB 3; Length 11 Pred. No. 2.2e-13; 0; Mismatches 5; Indels MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 Sequence 268, Application US/09991073 Patent No. US20020127576A1 GENERAL INFORMATION: Grimaldi, J. Christopher Gurney, Austin L. Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A Tumas, Daniel Query Match 31.9%; Best Local Similarity 88.6%; Matches 39; Conservative Ferrara, Napoleone Paoni, Nicholas F. Gerber, Hanspeter Gerritsen, Mary E Kljavin, Ivar J. APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. Botstein, David Goddard, Audrey Napier, Mary A. Desnoyers, Luc Eaton, Dan L. Godowski, Paul ò d

998-06-1 MBER: 60, 998-06-11 MBER: 60, 998-06-10, 998-06-10, 998-06-10, 998-06-10, MBER: 60,	06-19 06-60/09024 06-22 06-22 06-22 06-22 06-23 06-23 06-23 06-23 06-23 06-24 06-24 06-24	R: 60/09044 R: 60/09044 R: 60/09044 R: 60/09047 R: 60/09053 R: 60/09054 R: 60/09054 R: 60/09054 R: 60/09057 R: 60/09057	1998-06-25 NUMBER: 60/090695 1998-06-25 NUMBER: 60/090696 1998-06-25 1998-06-26 NUMBER: 60/090863 1998-06-26 NUMBER: 60/091360 1998-07-01 1998-07-02 NUMBER: 60/091478 1998-07-02 NUMBER: 60/091594 1998-07-02 NUMBER: 60/091519 1998-07-02 NUMBER: 60/091519 1998-07-02 NUMBER: 60/091519 1998-07-02 NUMBER: 60/091626 1998-07-02 NUMBER: 60/091638 NUMBER: 60/091638 NUMBER: 60/091638
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PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/08021
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08029
PRIOR APPLICATION NUMBER: 60/08032
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PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-10
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APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: Wood, William I.
APPLICANT: Screted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-24
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PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
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Pred. No. 2.2e-13;
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US-09-990-442-268
i Sequence 268, Application US/0990442
i Patent No. US20020132252A1
i GENERAL INFORMATION:
i APPLICANT: Ashkenazi, Avi J.
i APPLICANT: Baker, Kevin P.
i APPLICANT: Bocetein, David
     PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi,J.Christopher
Gurney,Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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31.9%;
Best Local Similarity 88.6%;
Matches 39; Conservative
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Eaton, Dan L.
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R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
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R FILING DATE: 1998-06-23
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R APPLICATION NUMBER: 60/090445
RR FILING DATE: 1998-06-24
RR APPLICATION NUMBER: 60/090472
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RR APPLICATION NUMBER: 60/090540
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RFILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/090694
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R APPLICATION NUMBER: 60/090695
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090696
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-27
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R APPLICATION NUMBER: 60/090542
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090676
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R APPLICATION NUMBER: 60/091544
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R APPLICATION NUMBER: 60/091519
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R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090444
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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31.9%; Score 198; DB 3; Length 117; 88.6%; Pred. No. 2.2e-13;

Query Match Best Local Similarity

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APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-11
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/05631
PRIOR APPLICATION NUMBER: 60/076945
PRIOR PILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/08322
PRIOR APPLICATION NUMBER: 60/08450
PRIOR APPLICATION NUMBER: 60/08460
PRIOR APPLICATION NUMBER: 60/08460
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PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-03
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Indels
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Patent No. US20020132253A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/088025
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Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Gerritsen, Mary E.
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39; Conservative
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PRIOR PELLING DATE: 1998-06-05
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/090252
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R PILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
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R APPLICATION NUMBER: 60/090355
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R FILING DATE: 1998-06-24
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Best Local Similarity 88.6%;
Matches 39; Conservative

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Gaps

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Length 117;

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R FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/088212
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APPLICATION UNMBER: 60/088655
FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/089908
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APPLICANT: Zhang, Zemin
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/93,604

CURRENT FILING DATE: 2001-11-14

PRIOR PEDLICATION NUMBER: 0/049787

PRIOR PEDLICATION NUMBER: 60/06250

PRIOR PELLING DATE: 1997-06-16

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PRIOR PELLING DATE: 1997-11-12

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PRIOR PELLING DATE: 1998-06-04

PRIOR PELLING DATE: 1998-06-04
                                  Sequence 268, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: ABMER, AVI J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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FILING DATE: 1998-06-04
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
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PRIOR PPLICATION NUMBER: 60/09163
PRIOR PPLICATION NUMBER: 60/09163
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Gaps ; 0 Length 117; Query Match
31.9%; Score 198; DB 3; Length 11
Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels

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2541, Ap
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Sequence 125, App
Sequence 4504, Ap
Sequence 5468, Ap
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Sequence 41125, A
Sequence 35, Appl
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Sequence 37295
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Perfect score:
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                                                                                                                                                                                                     Scoring table:
                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                               Searched:
                                                                                     Run on:
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Seguence 42105, A	Seguence 47061, A	Seguence 518, App	Seguence 34519, A	Sequence 39607, A	3747	Sequence 44082, A	Sequence 51140, A			Sequence 37358, A	Sequence 37988, A		Sequence 38265, A	Sequence 45252, A	Seguence 4048, Ap	Seguence 1, Appli	Seguence 44, Appl	Sequence 156, App	Sequence 3, Appli	
US-10-449-902-42105	US-10-449-902-47061	US-10-196-749-518	US-10-953-349-34519	US-10-449-902-39607	US-11-293-697-3747	US-10-449-902-44082	US-10-449-902-51140	US-10-449-902-53452	US-11-257-498-47	US-10-449-902-37358	US-10-449-902-37988	US-11-165-586-21	US-10-449-902-38265	US-10-449-902-45252	US-11-293-697-4048	US-11-181-115-1	US-11-181-115-44	US-11-105-233-156	US-11-306-504-3	
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104	918	1137	136	157	748	780	791	791	13	485	538	2074	478	838	268	303	303	303	307	
10.6	10.6	10.6	10.5	10.5	10.4	10.4	10.4	10.4	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.2	
65.5	65.5	65.5	65	65	64.5	64.5	64.5	64.5	64	64	64	64	63.5	63.5	63	63	63	63	63	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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APPLICANT: Fulurija, Alma
APPLICANT: Saudan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used the
FILE REPERENCE: 1700.0540001
CURRENT APPLICATION WINBER: US/11/257,498
CURRENT APPLICATION WINBER: 60/621,465
PRIOR APPLICATION NUMBER: 60/621,465
PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PARCHIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.9%; Score 198; DB 7; Length 117;
88.6%; Pred. No. 2.2e-14;
Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORVQVRPPHKAP
Sequence 6, Application US/11255699;
Publication No. US20060105393A1
GENERAL INFORMATION:
APPLICANT: APFEL, CHRISTIAN
APPLICANT: APFEL, THILO
APPLICANT: ZOFFMANN, SANNAH JENSEN
APPLICANT: PENSKL, MIREILLE
TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS
FILE REFERENCE: 22817
CURRENT FAPLICATION NUMBER: US/11/255,699;
CURRENT FILING DATE: 2005-10-21
PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 11
SOFFWARE: Patentin version 3.3
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-11-257-498-33
US-11-257-498-33
Sequence 33, Application US/11257498
Publication No. US20060088550A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.6
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-255-699-6
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APPLICANT: Bachmann, Martin F
APPLICANT: Bachmann, Martin F
APPLICANT: Suddan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FILE REPERENCE: 1700.0540001
CURRENT FILING DATE: 2005-10-25
PRIOR PILING DATE: 2005-10-25
PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.2
SEQ ID NO 42
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 1453
LENGTH: 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 VRPPHKA-PHVVPALPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSG-----RTWGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 75; DB 7; Length 28; 71.4%; Pred. No. 0.062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11453, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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                                                                                                                                                              ; Sequence 42, Application US/11257498; Publication No. US20060088550A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GSSFLSPEHQRVQVRPPHKAP 44
       24 GSSFLSPEHQRVQVRPPHKAP 44
                                             1 GSSFLSPEHOKVOORKESKKP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GSSFLSPEHQKVQQRKESKKP 21
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US-10-953-349-11453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 RVLNRLFPPSSR 102
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APPLICANT: Bachmann, Martin F
APPLICANT: Saudan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FILE REFERENCE: 1700.0540001
CURRENT FILING DATE: 2005-10-25
PRIOR APPLICATION NUMBER: 60/621,465
PRIOR RILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                              Sequence 30240, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, NICKOLAI et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: US/10/953,349

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT APPLICATION NUMBER: 2064-09-30

NUMBER OF SEQ ID NOS: 40552

SOFTWARE: PALENTI VERSION 3.3

SEQ ID NO 30240

LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 PPHKAPHVVP-----ALPLSNOLCDLE-QORHLWASVFSQSTKDSGSDLTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 12.2%; Score 75.5; DB 6; Length 135; Best Local Similarity 31.9%; Pred. No. 0.35; Matches 29; Conservative 5; Mismatches 24; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 75; DB 7; Length 28; 71.4%; Pred. No. 0.062; 5; Indels tive 1; Mismatches 5; Indels
                                                                                                                                      Query Match 12.6%; Score 78; DB 7; Length 28; Best Local Similarity 76.2%; Pred. No. 0.03; Matches 16; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 TGTW-----SSRRKS-----PSCSP 80
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                   24 GSSFLSPEHORVOVRPPHKAP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 40, Application US/11257498; Publication No. US20060088550A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 1 GSSFLSPEHORVOORKESKKP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
; SEQ ID NO 33
; LENGTH: 28
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-257-498-33
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ORGANISM: Felis catus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-30240
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APPLICANT: Bachmann, Martin F
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurija, Alma
APPLICANT: Saudan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used the FILE REPERENCE: 1700.054001
CURRENT APPLICATION NUMBER: US/11/257,498
CURRENT FILING DATE: 2005-10-25
PRIOR FILING DATE: 2006-10-25
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LTDHHHRLRSRAATAMAAAPHAYSSLVPVSAARPLSGSTVSFGASCHKWRKVPAWRLHC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 LSPEHORVQVR-----PPHKAPHVVP---ALPLSNQLCDLEQQRHLWASV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. VTEDEAEEVKDFGVNMALSMLKFYKREISPLLFSSCR-----YVPTCS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ----FSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQPSCS 114
                                                                                                                                                                                                                                                                                                                                                        Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                       40, Indels
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                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 72; DB 6;
24.8%; Pred. No. 1;
tive 14; Mismatches 40
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Pred. No. 0.17;
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; Publication No. US2006010537641
; GRNERAL INFORMATION:
    GRNERAL INFORMATION:
    TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION WUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; WUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Parentin Ver. 2.1
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; Sequence 34, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                 ; ORGANISM: Zea mays subsp. mays US-10-953-349-34518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 66.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.8%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-293-697-4423
                                                                                                                                                                                                     SEQ ID NO 34518
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APPLICANT: Saudan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FILE REFERENCE: 1700.054001
CURRENT APPLICATION NUMBER: US/11/257,498
CURRENT APPLICATION NUMBER: G0621,465
PRIOR APPLICATION NUMBER: 60621,465
PRIOR PILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SEQ ID NO 35
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSRERSRRSHQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 PSPSKSASLSALRSRGLQPGSLQSLQPAPRHDLGIKNSIIQANPVHPSIAALHAQTAPHQ 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 PISTPEALVKAKKRLSGALFSSSS----SSLT------LNTIASTSPSERAGMAHS 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQR-----VQVRPPHKA-----PHVVPAL 50
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-AO205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: US 2002-183870
PRIOR PLING DATE: 2002-15-10
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
12.0%; Score 74.5; DB 6;
Best Local Similarity 25.8%; Pred. No. 4.4;
Matches 32; Conservative 14; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 7;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34518, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/11257498 Publication No. US20060088550A1 GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GSSFLSPEHORVOVRPPHKAP 44
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Best Local Similarity 66.7%;
Matches 14; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Oryza sativa
US-10-449-902-41125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 PSCS 114
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US-10-953-349-34518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-257-498-35
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THE REPORT OF SEALTH

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Gaps

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(139)
OTHER INFORMATION: GI NO: 41400381
OTHER INFORMATION: NR Description: minus agglutinin [Chlamydomonas reinhardtii]
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LOCATION: (7)._(139)
OTHER INFORMATION: GI NO: 41400381
OTHER INFORMATION: NR Description: minus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (4).7(139)
OTHER INFORMATION: GI NO: 41400381
OTHER INFORMATION: NR Description: minus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (10)...(143)
OTHER INFORMATION: GI NO: 14253159
OTHER INFORMATION: NR Description: VMP3 protein [Volvox carteri f. nagariensis]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (7).-(161)
OTHER INFORMATION: GI NO: 41400381
OTHER INFORMATION: NR Description: minus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (7).-(148)
OTHER INFORMATION: IN Description: minus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description: minus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (4)._(143)
OTHER INPORMATION: GI NO: 30387315
OTHER INPORMATION: NR Description: unknown [Choristoneura fumiferana MNPV]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (5). (162)
OTHER INFORMATION: GI NO: 45190779
OTHER INFORMATION: NR Description: AER176Wp (Eremothecium gossypii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (7)..(139)
OTHER INFORMATION: GI NO: 12018149
OTHER INFORMATION: NR Description: gamete-
OTHER INFORMATION: specific hydroxyproline-rich glycoprotein
OTHER INFORMATION: [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (7). (139)
OTHER INFORMATION: PFAM Description: Extensin-like region
  TITLE OF INVENTION: FOR MODIFYING PLANT CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                             Seq. ID no. 13498251
                       FILE REFERENCE: 2750-2191PUS2
CURRENT PEPLICATION NUMBER: US/11/241,596
CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: 60/615,081
PRIOR FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 259
SEQ ID NO 129
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LCCATION: (7)..(162)
CTHER INFORMATION: 01 91400381
OTHER INFORMATION: NR Description:
                                                                                                                                                                                                                                                                           ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1). (164)
OTHER INFORMATION: Ceres
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34530, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-1291022
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
SOFTWARE: PATENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
SOFTWARE: PATENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
SOFTWARE: PATENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
SOFTWARE: PATENT APPLICATION NUMBER: US/10/953,349
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; Publication No. US20060134786A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Kenneth A.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL
                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LLTSSPWPPSPLPPSPPLPSPHQRQPAPWSEGGPSPCAPLSARPPAPPWQWLPAPCLPA 62
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                                                                                                                                                                                                                                              3 SPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVVPALPLSNQLCDLEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LLLGMLWLDLAMAGSSFLSPEHOR------VQVRPPHKAP-----HVVPA
                                                                                                                                                                                                Gaps
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LOCATION: (146)...(146)

CTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-953-349-34530
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                                                                                                                                                                                                                                                                                                                                                          63 RHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPPSSR-ERSRRSHQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                 222 ----SSSLSPYVKSSSSH------NEVFLPGSRGPRRRKSKQ 253
                                                                                                                                        DB 7; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.3%; Score 70; DB 6; Length 164; 24.8%; Pred. No. 1.7; tive 9; Mismatches 52; Indels
                                                                                                                                                                                             Indels
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                                                                                                                                   Query Match
11.4%; Score 70.5; DB 7; I
Best Local Similarity 30.3%; Pred. No. 3.2;
Matches 33; Conservative 9; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 LPLSNOLCDLEQORHLWASVFSOSTKD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 ASTPPRSRRRSTSTROARPXPSPSP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (109)...(109)
OTHER INFORMATION: Xaa can be any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
LOCATION: (134)
OTHER INFORMATION: Xaa can be any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.8
Matches 36; Conservative
                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4423
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US-10-953-349-34530
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LENGIH: 307
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nagariensis]
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NAME/KEY: misc_feature
LOCATION: (6).7(161)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin (Chlamydomonas reinhardtii)
                          LOCATION: (3). [160)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin (Chlamydomonas reinhardtii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (3)._[(161)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (6). 7(160)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (6).-1(161)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (6)...(161)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VPWPRRCC------WAQATAGSSSSPASSPSRPATPSHSRTTPASRTTSSSTKTRCRA 113
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: LOCATION: (9)..(145)

: OTHER INFORMATION: GI NO: 14253159

: OTHER INFORMATION: NR Description: VMP3 protein [Volvox carterians.]

US-11-241-596-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
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Publication No. US20060105376A1
GENERAL INPORMATION:
TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SERGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.1%; Score 69; DB 'Best Local Similarity 24.8%; Pred. No. 2.2; Matches 36; Conservative 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 --FPPSSRERSRRSHQ----PSCSP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 ASTPPRSRRRSTSTRQARPTPSPSP 138
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CORGANISM: Homo sapiens
US-11-293-697-4504
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US-11-293-697-4504
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Sequence 125, Application US/11241596
Publication No. US20060134786A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Kenneth A.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES AND POLYPEPTIDES CURRENT TITLE OF INVENTION: NUMBER: US/11/241,596
CURRENT APPLICATION NUMBER: US/11/241,596
CURRENT PILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: 60/615,081
PRIOR FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 259
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LOCATION: (6).7(161)
OTHER INFORMATION: GI NO: 41400384
OTHER INFORMATION: NR Description: plus agglutinin [Chlamydomonas reinhardtii]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (3)..(142)
OTHER INFORMATION: GI NO: 30387315
OTHER INFORMATION: NR Description: unknown [Choristoneura fumiferana MNPV]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LLTSSPWPPSPLPPSPPLPSPHQRQPAPWSEGGPSPCAPLSARPPAPPWQWLPAPCLPA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VOVRPPHKAP-----HVVPA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SGSDLTVSGRTWGLRVLNRL-- 96
                                                                                                                                                                                                                                                                                                                                                                                             48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (b)..(138)
OTHER INFORMATION: GI NO: 12018149
OTHER INFORMATION: GN Description: gamete-
OTHER INFORMATION: specific hydroxyproline-rich glycoprotein a2
OTHER INFORMATION: (Chlamydomonas reinhardtii)
                                                                                                                                                                                                                                                                                                                                     7; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                             52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ION: (6). (138)
INFORMATION: PFAM Description: Extensin-like region
                                                       FEATURE:
NAME/KEY: misc_feature
LOCATN: (134)..(134)
OTHER INFORMATION: Xaa is any aa, unknown or other
                                                                                                                                                              FEATURE:

NAME/KEY: misc feature

LOCATION: (146)... (146)... (146)... OTHER INFORMATION: Xaa is any aa, unknown or other US-11-241-596-129
LOCATION: (109)..(109)
OTHER INFORMATION: Xaa is any aa, unknown or other
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INFORMATION: Ceres Seq. ID no. 12404085
                                                                                                                                                                                                                                                                                                                               Query Match
11.3%; Score 70; DB 7
Best Local Similarity 24.8%; Pred. No. 1.7;
Matches 36; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LLLGMLWLDLAMAGSSFLSPEHQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 LPLSNQLCDLEQQRHLWASVFSQSTKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 --FPPSSRERSRRSHQ----PSCSP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays subsp.
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LOCATION: (6)..(138)
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LOCATION: (3)..(142)
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us-10-659-782b-32.rapbn

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Query Match 11.0%; Score 68.5; DB 7; Length 365; Best Local Similarity 27.5%; Pred. No. 6.4; Matches 22; Conservative 7; Mismatches 34; Indels 17; Gaps
                                                                                                                                                                                            Search completed: July 11, 2006, 17:21:07 Job time : 22 secs
                                                                                                                 96 LFPPSSRERSRRSHQPSCSP 115
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282 -YPPS-----AHPPTLPP 293
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415-110-659-7826-11 com 112

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Run on:	July 11, 2006, 16:23:31 ; Search time 27.9 Seconds (without alignments) 1725.623 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-659-782B-11_COPY_112_462 644 1 atgcctcccagggaccgtcaagctgcagcccgagctc 351
Scoring table:	BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
Searched:	2589679 seqs, 457216429 residues
Total number of	Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abss/ABS/BBS spool/US10659782/runat\_11072006\_110906\_1994/app\_query.fasta\_1
-DB=A\_Geneseq -QFMT=fastan -SUFFTX=n2p.rag -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LISTA-45
-UORALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTENT=pcto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10659782\_GCGN 1 1 364 @runat 11072006\_110906\_1994 -NOPU=6 -ICPU=3
-NO\_WMAP -NGS\_GCRES=0 -WALT -DSPBLOCER=100 -LONGLOG -DEV\_TIMEOUT=120
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Database :

geneseqp2003bs:\*geneseqp2004s:\* geneseqp20028:\* geneseqp2003as:\* geneseqp2006s:\* A\_Geneseq\_8:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2000s:\* geneseqp20018:\* geneseqp2005s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

uon	Ady78074 Human ghr	Human ghr	Human exo	Protein d	Human sig	Aab20101 Zsig33 pr	Human zsi	Human pol
Description	Ady78074	Adk66754	Aae33410 H	Aaw87991	Aay87236	Aab20101	Aab62649	Aam38890
ΩI	ADY78074	ADK66754	AAE33410	AAW87991	AAY87236	AAB20101	AAB62649	AAM38890
DB	٥	ω	9	~	ო	4	4	4
% Query Match Length DB	116	9	91	117	117	117	117	117
% Query Match	94.0	31.7	31.7	31.7	31.7	31.7	31.7	31.7
Score	605.5	204	204	204	204	204	204	204
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AAB60511 ABB78319 AAE23838 AAE15883 ABU58046	ABU82636 ABU82636 ABU60555 ABU13937 ABU81090 ABU72522	ABUS 9871 ABUS 9871 ABUS 9868 ABUS 98977 ABUS 98977 ABUS 355 AAE 3409 ABUS 7006 ABUS 7006 ABUS 7006 ABUS 7006	ABU10892 ABU81644 ABU86893 ABO34097 ADA45961 ADA19042 ADA5392 ADA51991 ADB27991 ADB6470 ADB6470 ADB66470 ADB66470 ADB66470
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## ALIGNMENTS

Diagnosis; obesity; anorectic; nutritional disorder; diabetes; antidiabetic; endocrine disease; metabolic disorder; gastrointestinal disease; drug screening; gene therapy; ghrelin. Human ghrelin variant 2 protein, SEQ ID NO: 32. Key Location/Qualifiers Misc-difference 64. .65 /note= "Encoded by CATCTCTGG" ADY78074 standard; protein; 116 AA. (first entry) Homo sapiens. 02-JUN-2005 ADY78074; RESULT 1 ADY78074 XIXAXXBXXBXXIIIIX

US2005059015-A1.

17-MAR-2005.

11-SEP-2003; 2003US-00659782

11-SEP-2003; 2003US-00659782

(MINT/) MINTZ L.

Mintz L;

Screening animals (i.e. pigs) to determine those more likely to produce desired growth, appetite and fatness to optimize breeding and selection techniques comprises detecting the presence of a polymorphism in the

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Anderson

Kim K,

Rothschild MF,

WPI; 2004-010667/01.

14-NOV-2002; 2002US-00294191 14-NOV-2001; 2001US-0333222P

ROTHSCHILD M KIM K. ANDERSON L L.

(KIMK/) (ANDE/) Disclosure; SEQ ID NO 3; 24pp; English.

Ghrelin gene.

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                                                                                                                                                                                          and/or diabetes related genes and their corresponding proteins. The invention also relates to compositions, reagents, kits and methods for diabetes, more treating obesity and/or diabetes. The composition and methods are useful for diagnosing, monitoring and treating obesity and/or diabetes. These may also be used in drug screening purposes and in gene therapy. The present sequence is the human shrelin (GHRL) variant protein. This protein is encoded by an obesity and diabetes related gene.
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                                                        New isolated nucleic acid and encoded amino acid sequences useful for diagnosing, monitoring and treating obesity and/or diabetes, or in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG
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                                                                                                                                                                                obesity
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                                                                                                                                                                              invention relates to alternative splice variants of
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116
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                        Claim 32; SEQ ID NO 32; 74pp; English
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605.50
99.1%
99.1%
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2005-240894/25
                                                                                                    screening purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     appetite;
                    N-PSDB; ADY78053
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 116 AA;
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Pred. No.:
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The present invention relates to a method of screening animals to determine those more likely to produce desired growth, appetite and fatness which involves obtaining a sample of genetic material from the animal and assaying for the presence of a genotype in the animal which is associated with favourable growth, appetite and fatness, the genotype characterised by a polymorphism in the ghrelin gene. The composition and methods are useful in screening animals (i.e. pigs) to determine those more or less likely to produce desired growth, appetite and fatness to optimise breeding and selection techniques. The present sequence is human ghrelin protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln---
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204.00
44.1$
43.2$
31.7$
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Query Match:
                                                                                                                                                                                                                                             Sequence 60 AA;
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AAE33410
ID AAE3
XX
AC AAE3
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The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypoptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient carymes, gastrointestinal inflammation, reflux disease and nutrient carymes, gastrointestinal inflammation, reflux disease and nutrient carymes, gastrointestinal inflammation, reflux disease con nutrient carymes protein motilin belongs has been associated with neurological complexity and other metabolic disorders where neurological treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33 agonists, antagonists and ligands and to produce antibodies
                                                                                                                                                                                                                                                                                     Zsig33; gastric motility; gastrointestinal inflammation; reflux disease; nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility.
                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/note= "signal peptide"
24. .117
/note= "mature protein"
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                                                                                                                                AAW87991 standard; protein; 117 AA
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97US-00822897
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44.1%
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                                                                                                                                                                                                                                                 Protein designated zsig33.
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N-PSDB; AAX04550.
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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24-MAR-1997;
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                                                                                                                                                                      AAW87991;
                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                            AAW87991
                                                                                             RESULT
                                                                                                                                                    181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exonal deleted preproghrelin and/or a GHS-R lb proteins or nucleic acids. The antibodies, exon 3-deleted form of preproghrelin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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                                                                     Ghrelin, preproghrelin, GHS-R 1b, benign prostatic hyperplasia, therapy, breast, cervical, uterine; choriocarcinoma; prostate; ovary, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln-----
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                                 Human exon 3-deleted ghrelin protein.
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                                                                                                                                                                                                                                                                                                     10-MAY-2001; 2001AU-00004919.
17-DEC-2001; 2001AU-00009567.
                                                                                                                                                                                                                                                               10-MAY-2002; 2002WO-AU000582
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02-APR-2003 (first entry)
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N-PSDB; AAD50726.
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Best Local Similarity:
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                                                                                                                                                                                      WO200290387-A1.
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                                                                                             breast; cervic
cancer; human.
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Claim 1; Page 168-169; 327pp; English
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                                                                     GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAAGACCTCCC 120
                                                                                                             121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
                                                                                                                                                                                            241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
                                                                                                                                                                                                                                                                                                                                                                           Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; noctropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia; asthma; Crohn's disease; infection; Allaheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR;
R, Hillman JL;
                             Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
                                                                                                                                                                                                                                   301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT
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H, Patterson C, Reddy R,
          US-10-659-782B-11_COPY_112_462 (1-351) x AAW87991 (1-117)
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m IE, Au-Young J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscular dystrophy
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01-OCT-1998;
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anticancer, anti-inflammatory, anticobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. Hypps can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, cathma, Crohm's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, solizophrenia, ovulatory defects, muscular dystrophy). HSPP chick diseases, solizophrenia, ovulatory defects, muscular dystrophy), detecting HSPP in stendard hybridisation and amplification assays (for detecting HSPP in stendard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists, in competitive drug screens, and for purification of HSPP from natural
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Query Match:
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(first entry)
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N-PSDB; AAF83678.
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                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                    23-JUL-2001
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                                                                                                                                                                                            AAB62649;
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Peptide
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                                                                                                                                                                                The present sequence is that of zsig13, a secreted protein with homology to motilin (see AAB20102). Zsig13 is expressed at high levels in the small stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig13, termed SGIP (see AAB20100), is claimed. SGIP is a ligand for growth hormone secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum tissue, modulating pancreatic secretion of hormones and digestive enzymes, inducing growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                        in duodenum
SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel variants of SGIP peptides for modulating contractility in do or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating gastric
                                                                                                                                                                  is claimed in Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone secretion, and modulating gastric emptying
                                                                                                                                                                                                                                                                                                                          Bishop PD;
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Mismatches:
Indels:
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Matches:
                                                                       Location/Qualifiers
1. .23
(label= Signal_peptide 24. .117
(label= Mature_protein
                                                                                                                                                                                                                                                                                                                          Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                     SGIP_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; 54; 61pp; English.
                                                                                                                                                                                                                                                                       99US-00345157.
                                                                                                                                                                                                                                             2000WO-US018306.
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                                                                                                                                      24. .34
/label= 8
/note= "t
                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-123010/13.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 117 AA;
                                                                                                                                                                                            WO200100830-A1
                                                  Homo sapiens
                                                                                                                                                                                                                                                                       30-JUN-1999;
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                                                                                                                                                                                                                                              30-JUN-2000;
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                                                                                      Peptide
                                                                                                                Protein
                                                                                                                                          Peptide
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receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AABGZ449), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, compared in contractility, nutrient uptake, secretion of digestive and parcreatic enzymes and hormones, secretion of insulin-like growth factor or secretion of non-zsig33 proteins. It is useful for modulating growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, cremodeling, iow osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, grotein catabolic responses after surgery, cachexia, protein loss, darrism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated
241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
                                                                                             -- 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
24. .37
/note= "specifically claimed fragment that binds to the
GHS-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastric contractility, nutrient uptake, digestive; pancreatic, human, insulin-like growth factor-I; growth hormone, bone, gastrointestinal, glucose, osteopathic, anorectic, vulnerary, immunomodulator, GHS-R, G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide.
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                                                                                                                                                                                                                                                                         52
                                                                                                                                                                                      301 AGCAGAGAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT
                                                                                                                                                                                                                                       Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deisher TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62649 standard; protein; 117 AA
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29-NOV-2000; 2000US-00727344
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                                  Tang YT,
Wang J,
Zhou P,
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DB:
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                                                                                                                                                                                                                                                      181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
                                                                                                                                                                                                                                                                                          241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
                                                                                                                                                     37
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        release in a mammal. The present sequence represents the human zsig33 polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                          and stimulating glucose-induced insulin
                                                                                                                                                                                                                                                                                                                              350
                                                                                                                                                                                                                                                                                                                            AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 2035.
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2000US-00620312.
2000US-00653450.
2000US-00662191.
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2000US-00488725.
2000US-00552317.
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gastrointestinal disorders,
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                                                                                    Best Local Similarity:
Query Match:
DB:
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                                                                            Percent Similarity:
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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21-JAN-2000;
25-APR-2000;
                                  Sequence 117
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                                                  Alignment Scores:
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressont and eyfoctatic activity. The polymocleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous such as ystem, such as peripheral nervous injuries, peripheral nervous disease, such as localised neuropathies and central nervous system disease, such as a lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic cutilisation of the activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                   Ren F, Wang D;
Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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                                                   Qian XB,
Yang Y,
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Conservative:
Mismatches:
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Α,
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                                                   Chen R,
Xu C,
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                                                Asundi V, Chen
Wehrman T, Xu (
R, Drmanac RT;
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N-PSDB; AAI58046.
                                             Liu C, Wang Z, WGoodrich
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Best Local Similarity:
(HYSE-) HYSEQ INC
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181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
                                                                           241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides; vectors and host cells comprising such DNA, a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention; and an assay and kit for detecting the peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
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                                                                                                                                                                                                                                                                                                                                                                     New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis of infant growth disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder;
                                                                                                                                                                                                                                                                                                      Hosoda H, Matsuo H, Minamitake Y;
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Matches:
Conservative:
Mismatches:
                                     Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 182; 210pp; Japanese.
                                                                                                                                                                                                                      23-JUL-1999; 99JP-00210002.
29-NOV-1999; 99JP-00338841.
26-APR-2000; 2000JP-00126623.
                                                                                                                                                                                               24-JUL-2000; 2000WO-JP004907
             (first entry)
                                                                                         growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%
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N-PSDB; AAF59645.
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Best Local Similarity:
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                                                                                                                                            WO200107475-A1
                                                                                                                   Homo sapiens
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The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP SGIP and all assays to identify modulators of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antigonists may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used as diagnostic agents for detecting the presence of SGIP in samples
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301 AGCAGAGAAAGGAGTCGAAGAAGCCAGCCAAGCTGCAGCCCCGAGCT 350
                                              ----ArglysGluSerLysProProAlaLysLeuGlnProArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Short gastrointestinal peptide; SGIP; zsig33; motilin.
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/note= "signal peptide"
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/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human zsig33.
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N-PSDB; ABV72214.
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uptake; growth hormones, secretion of digestric contractility, nutrient uptake; growth hormones, secretion of digestrive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probables in diagnosis cassays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in need of restorative therapy. The ZSIG33 peptides are used as antigens in need of restorative therapy. The ZSIG33 peptides are used to down regulate expression and activity. The modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the conditate gastric contractility, nutrient uptake, growth hormones, the condition of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the panoreas. ZSIG33-like peptide is used in protein therapy. The present sequence is home.
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Best Local Similarity:
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(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
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N-PSDB; AAD38238.
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linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon

peptides and nucleic acid molecules encoding such zsig33-like peptides.

ZS33LP peptides activate the immune system in boosting immunity because infectious diseases, treating immunocompromised patients such as human infectious diseases, treating immunocompromised patients and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and isolate receptors involved in growth regulation in the liver; blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or cyclerations containing glucose and as adsorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the insulin release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. ZS33LP peptides, nucleic acids and/or antibodies are useful for treating disorders associated with gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy. The present sequence is human zsig33 protein
                                                                                                  /note= "Human mature zsig33 protein"
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                                          1. .23
/label= Signal_peptide
24. .117
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                   Location/Qualifiers
                                                                                                                                                                                                                         10-MAY-2001; 2001WO-US015091.
                                                                                                                                                                                                                                                                11-MAY-2000; 2000US-00569271.
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                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC
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Peptide
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Length:
Matches:
Conservative:
Mismatches:
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2.23e-13
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31.7%
                    Percent Similarity:
Best Local Similarity:
                                         Query Match:
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121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
                                                                      181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
                                                                                                                241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
                                                                                                                                                                                                                                                                                                           Human, PRO, cytostatic, tumour, cancer, breast, lung, stomach, liver,
horse, cow, dog; cat, sheep, pig, goat, rabbit, ADEPT,
antibody-dependent enzyme mediated prodrug therapy.
                                                                                                                                                        301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAAGCTGCAGCCCGAGCT 350
                                                                                                                                                                    ABU58046 standard; protein; 117 AA.
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97US-0062250P.
97WO-US020069.
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98US-0088742P
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24-NOV-1997;
25-FEB-1998;
20-MAR-1998;
28-APR-1998;
07-MAY-1998;
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17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 18-AUG-1998; 18-AUG-1998; 18-AUG-1998; 18-AUG-1998; 26-AUG-1998; 16-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1998; 17-SEP-1999; 17-SEP-1999; 17-SEP-1999; 17-SEP-1999;

08-MAR-1999; 12-MAR-1999; 23-JUN-1999; 23-JUN-1999; 26-JUL-1999; 26-JUL-1999; 26-JUL-1999; 26-JUL-1999; 30-NOV-1999; 30-NOV-1999; 30-NOV-1999; 30-NOV-1999; 30-NOV-1999; 30-NOV-1999; 30-MAR-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 25-MAR-2000; 30-MAR-2000; 30-MAR-2000; 30-MAR-2000; 310-MAR-2000; 310-MAR-200 and the properties

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98US-0088738P.
98US-0088742P.
98US-0088810P.
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18-FEB-2000;
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15-SEP-1999
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                                                                                                                                                                                                                                                                                                CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAAACAGACTGTTTCCCCCTTCC 300
                                                                                                                                                Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                                                                                                                                      301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAAGCTGCAGCCCCGAGCT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted or transmembrane protein PR01066.
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                                                                 Conservative:
Mismatches:
Indels:
                                                Length:
Matches:
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97US-0062250P.
97WO-00520069.
97US-0065186P.
97US-0065311P.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
07-SEP-2000; 2000US-0230978P.
                                           2.23e-13
204.00
44.18
43.28
31.78
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                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                     Alignment Scores:
Pred. No.:
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13-NOV-1997;
24-NOV-1997;
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05-NOV-1997
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US-10-659-782B-11\_COPY\_112\_462 (1-351) x ABU59124 (1-117)

121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180

181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAAGGACTCTGGGTCTGAC 240

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241 CTCACTGTTTCTGGAAGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300

301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350 

ABU82636 standard; protein; 117 AA

38

RESULT 15 ABU8263 26-JUN-2003 (first entry)

ABU82636;

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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in complete a broadcaive molecule to a cell expressing a PRO polypeptide, and in modulating a bioactive molecule to a cell expressing a PRO in modulating at least one biological activity of a cell expressing a PRO converse broadcar and expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO154 and PRO186 conseculation of pro343, PRO828, PRO826, PRO826, PRO186 or PRO1360 and PRO1387 induce c-fcs in endothelial growth, and PRO136, CC PRO1360 and PRO1387 induce c-fcs in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular conditions are accorders where angiogenesis would be conditionally accoliferation of colls and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting endothelial cell growth in colls and is thus useful for inhibiting endothelial cell growth in colls and is thus useful for inhibiting tumour growth. PRO826, PRO1068, PRO1068 or PRO1132 enhance survival/proliferation of stimulated T-lymphocytes and are therapeutically useful for renating retinal imminities, e.g. retinities plamentosum, AMD. PRO819, PRO813 and therefore associated with dermatitis, herpetiformis or Crohn's comphropathies associated with dermatitis, herpetiformis or Crohn's comphropathies associated with dermatitis, herpetiformis or crohn's colliferation and/or redifferentiation of chondrocytes in culture and are disease. PRO81310, PRO844, PRO8132, PRO8132, and arthritis. This is the amino acid sequence of a novel human PRO protein
                                                                                                                                                                                                                                                                                                                                                                                 J, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
ewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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                                                                                     23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOY-2000; 2000WO-US030552.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
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29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
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                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Roy MA, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-247083/24.
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30-MAY-2000;
02-JUN-2000;
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11-AUG-2000;
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Zhang Z;
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cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; crohn's disease; sports injury; arthritis.
                                                                        Human; PRO; secreted protein; transmembrane protein;
                                                     Human secreted/transmembrane protein PRO1066.
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97WO-US020069.
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07-MAY-1998;
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Mismatches:
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Gaps:
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Best Local Similarity: Query Match: DB:

Percent Similarity:

Alignment Scores:

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121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
                                                                                                                                                                                                                                                                                                 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
                                                                                                                                                                                                                                                                                                                                     241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
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51
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66
                                                                                                                                                                   US-10-659-782B-11_COPY_112_462 (1-351) x ABU82636 (1-117)
                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                  Gaps:
30-MAR-2000; 2000WO-US008439.

17-MAY-2000; 2000WO-US01358.

17-MAY-2000; 2000WO-US013705.

22-MAY-2000; 2000WO-US014941.

30-MAY-2000; 2000WO-US015264.

23-JUN-2000; 2000WS-0213637P.

28-JUL-2000; 2000WS-US020317.

11-AUG-2000; 2000WO-US02031.
                                                                                                 2.23e-13
204.00
44.1$
43.2$
31.7$
                                                                                                            Score:
Percent Similarity:
4
Best Local Similarity:
4
Query Match:
6
                                                                                          Alignment Scores:
Pred. No.:
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Search completed: July 11, 2006, 16:28:20 Job time : 141.5 secs

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(without alignments)
1717.225 Million cell updates/sec
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                                                                                                                   July 11, 2006, 16:28:41 ; Search time 5.9 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                            protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           US-10-659-782B-11_COPY_112_462
644
                                                                                                                                                                                                                                                                                                                                                                                            283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                              0.5
7.0
7.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                             Title:
Perfect score:
Sequence:
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                                                                            OM nucleic
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                                                                                                                   Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Command line parameters:
-MODEL=frame+ n.Dp. model - DEV=xlp
-MODEL=frame+ n.Dp. model - DEV=xlp
-MODEL=frame+ n.Dp. model - DEV=xlp
-De\_abss/BREB spool/USI0659782/runat\_11072006\_110911\_2052/app\_query.fasta\_1
-De\_abss/BREB\_spool/USI0659782/runat\_11072006\_110911\_2052/app\_query.fasta\_1
-DB-ETR - OFMT=fastan - SUFFIX=n.Dp. rpr - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
- UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
- UNCALIGN=200 - TRR\_SCORE=pct - TRR\_MAX=100 - TRR\_MIN=0 - ALIGN=15 - MODE=LOCAL
- USER=USI0659782\_@CGN 1 1 63\_@runat\_11072006\_110911\_2052 - NCPU=6 - ICPU=3
- NO\_WMAP - NGG\_SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG - DEV\_TIMEOUT=120
- WARN\_TIMEOUT=10 - THREADS=1 - XGAPPOP=10 - XGAPEXT=0.5 - FGAPPOP=6 - FGAPEXT=7
- YGAPDF=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	204	31.7	117	¦ ⊣	A59316	qhrelin precursor
8	165	25.6	117	-	B59316	ghrelin precursor
m	85.5	13.3	3164	-4	ммвене	UL36 protein - hum
4	85	13.2	135	~	S12549	hypothetical prote
Ŋ	84	13.0	317	~	A28996	proline-rich prote
9	83	12.9	334	н	TVMSJA	transcription fact
7	83	12.9	334	7	S12742	transcription ,fact
ω	82	12.7	383	~	S32975	gene BCRF2 protein
0	81	12.6	141	7	E72594	hypothetical prote
10	80.5	12.5	381	7	S16506	hypothetical prote
11	80.5	12.5	206	7	B56201	transcription fact
12	80.5	12.5	514	7	A56201	transcription fact
13	80.5	12.5	744	~	T35192	probable ABC trans
14	80	12.4	1056	7	G84865	hypothetical prote

MHC class III hist	ine-rich p	class II	Ξ	regulator of nucle	transcription fact	transcription fact	neural cell adhesi	myocyte enhancer f	gene LF3 protein -	hypothetical prote	hypothetical prote	hypothetical diver	mucin 1 precursor,	atrophin-1 - human	KIAA0641 protein -	proline-rich prote	unconventional myo	unconventional myo	bcsA 5'-region pro	ap-1-like transcri	LRGS protein - Chl	thyrotropin recept	homeotic protein H	myocyte enhancer f	protein-tyrosine k	folate-binding pro	probable sugar kin	nitrite reductase		collagen alpha 2(I
B35098	A24264	S37671	836152	AG0449	S15664	JC5805	IJMSNI	JC5881	\$27923	T48627	T25894	T38459	S10571	G01763	T00378	D29149	A59295	A59266	B36963	T50109	T08179	148882	A39724	JC5882	833596	BFBO	AE0941	A49848	S50832	CGHU2S
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2142	240	1870	1872	136	544	718	1115	349	924	530	1217	1794	347	1184	1207	188	3511	3530	353	552	640	764	320	339	1001	222	530	1176	1184	1366
12.3	12.2	12.2	12.2	12.1	12.1	12.1	12.1	12.0	12.0	11.9	11.9	11.9	11.8	11.8	11.8	11.7	11.7	11.7	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.5	11.5
79.5	78.5	78.5			78	78	78	77.5	77.5	76.5	76.5	76.5	16	16	9/	75.5	75.5	75.5	75	75	75	75	4.	•	74.5	74	74	74	74	74
15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

ghrelin precursor - human N;Alternate names: preproghrelin C;Species: Homo sapiens (man) C;Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 09-Jul-2004 C;Accession: A59316 R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K. Nature 402, 656-660, 1999 A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach. A;Reference number: A59316; MUD:20067959; PMID:10604470

A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-117 <KOJ>

A; Cross-references: UNIPROT: Q9UBU3; UNIPARC: UP100000162D3; GB:AB029434; NID:g6691571; PiA; Experimental source: tissue stomach endocrine cells
A; Experimental source: tissue stomach endocrine cells
A; Note: submitted to GenBank, June 1999
C; Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (grow C; Superfamily: motilin
C; Keywords: hormone; lipoprotein; stomach
F; 1-23/Domain: signal sequence #status predicted <SIG>F; 2-117/Domain: signal sequence #status predicted \*MAT>
F; 2-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>F; 2-117/Domain: carboxyl-terminal propeptide #status experimental

1117 51 1 0 66 Conservative: Mismatches: Indels: Length: Matches: 2.06e-12 204.00 44.1% 43.2% 31.7% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

US-10-659-782B-11\_COPY\_112\_462 (1-351) x A59316 (1-117)

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M. J. 15 W.

Qy 241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300	301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCGAGCT 350 	RESULT 3 WMBEH6 UL36 procein - human herpesvirus 1 (strain 17) C.Shecies: human herpesvirus 1	C.Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004 C.Accession: 130088	A, Gen. Virol. 69, 1531-1574, 1988 A,Title: The complete DNA sequence of the long unique region in the genome of herpes A,Reference number: A30083; MUID:88274327; PMID:2839594 A,Accession: 130083 A,Status: nucleic acid sequence not shown; translation not shown	A;Molecule type: DNA A;Residues: 1-3164 <mcg> A;Kesidues: 1-3164 <mcg> A;Cross-references: UNIPROT:P10220; UNIPARC:UP10000136B9B; GB:X14112; NID:g1944536; PIDN C;Genetics: C;Genetics: A;Gene: U136 C;Superfamily: varicella-zoster virus gene 22 protein</mcg></mcg>	Alignment Scores: Pred, No.: 1.81 Length: 3164 Score: 85.50 Matches: 37	cent Similarity: 37.2% Conservative: st Local Similarity: 27.0% Mismatches: sry Match: 13.3% Indels:	DB: US-10-659-782B-11_COPY_112_462 (1-351) x WMBEH6 (1-3164)	Qy 9 CCCAGGGACCGTCTGCAGCCTCCTGGCATGCTCTGGCTGG	Qy 69 AGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACC 116	Qy 117 TCCCCACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTG 170	Qy 171 TGACCTGGA 179 	Qy 180 GCAGCAGCCATCTGGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGA 239	Qy 240 CCTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTC 299	Qy 300 CAGCAGAGAAAGAGTCGAAGAGCCACCAAGCTGCAGCTCCGGG 348 ::: ::	RESULT 4 \$12549 hypothetical protein - human herpesvirus 4 \$1,2549 c); Species: human herpesvirus 4, Epstein-Barr virus \$1,5pecies: human herpesvirus 4, Epstein-Barr virus \$2,5pecies: 13-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004 \$2,Accession: \$12549
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20 Qy 61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120	21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnGln	DB 37	241 CTCACTGTTTCTGGAAGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC	Db 37 37  Qy 301 AGCAGAGAAAGGAGTCGAAGACCACCAGCCAAGCTGCAGCCCCGAGCT 350	RESULT 2 B59316 Ghrelin precursor - rat Shrate names: preproghrelin C:Species: Rattus norvegicus (Norway rat)	C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004 C;Accession: B59316 R:Kojima, M.; Hoooda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K. Natinte 402 656.660	A;Title: Girelin is a growth-hormone-releasing acylated peptide from stomach. A;Reference number: A59316; MUID:20067959; PMID:10604470 A;Accession: B59316		A;Cross-references: UNIPROT:Q9QYH7; UNIPARC:UPI000012B411; GB:AB029433; NID:g6691569; PI A;Experimental source: strain SD; tissue sromach endocrine cells A;Note: submitted to GenBank, June 1999 C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt	C:Superfamily: motilin C:Keywords: hormone; lipoprotein; stomach F:1-23/Domain: signal sequence #status predicted <sig> F:24-51/Product: ghrelin #status predicted <mat></mat></sig>	F;52-117/Domain: carboxyl-terminal propeptide #status predicted <ctp> F;26/Binding site: octanoate (Ser) (covalent) #status experimental Alignment Scores:</ctp>	Pred. No.: 1.78e-08 Length: 117 Score: 165.00 Matches: 43 Percent Similarity: 39.8\$ Conservative: 4 Bust Local Similarity: 36.4\$ Mismatches: 5 Dubry March: 75.6\$	Y_112_462 (1-351) x B59316 (1-117)	Oy 1 ATGCCTCCCCAGGGACCGTCTGCAGCCTCCTGGCATGCTCTGGCTGG	Qy     61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120	Qy 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180  Db 35 35  Qy 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240

13.0% Indels: 21 2 Gaps: 3 -11_COPY_112_462 (1-351) x A28996 (1-317)  CCTCCCCAGGGACCGTCTGCAGCCTCCTCCTCCTCGGCATGCTCTGGCTCGACT 58	TGGCCATGGCAGCTCCAGCTTCCTGAACACCAGAGAGTCCAGGTGAGACTC 118	AGCAGCACCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAGGACTCTGGGTCTG 238	protein; protein PEA1; transcription factor, TGAC 31-Dec-1989 #text_change 09-Jul-2004 -8467, 1988 jun by serum growth factors.	204; PMID:3186736 IPARC:UPI0000019B4; GB:J04115; NID:g192577; PIDN rsi, P.; Verma, I.M. UN/AP-1 by serum and TPA. 467; PMID:2457172	A; Accession: S0463 A; Molecule type: mRNA A; Residues: 1-314 <lam> A; Residues: 1-314 <lam> A; Cross-references: UNIPARC: UPI00000019B4; EMBL: X12740; NID: 952762; PIDN: CAA31236.1; PI: R; Ryseck, R.P.; Hirai, S.I.; Yaniv, M.; Bravo, R. Nature 334, 535-537, 1988 A; Title: Transcriptional activation of c-jun during the G(0)/G(1) transition in mouse f A; Reference number: S04537; MUID: 88302446; PMID: 3136397 A; Molecule type: mRNA</lam></lam>	E62; EMBL:X12761; NID:g52758; PIDN:CAA31252.1; PII n; fos/jun DNA-binding domain homology r; phosphoprotein; proto-oncogene; transcription domain homology «FJD»  Length: 334  Matches: 23
Query Match: DB: US-10-659-782B Oy 5	Qy         59 TGGCCATGGCAGGCTCCAGCTTCC	Qy 179 AGCAGCAGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACA	RESULT 6  TUMSJA  transcription factor AP-1 - mouse  N.Alternate names: fos-associated 39K 19 C;Species: Mus musculus (house mouse) C;Date: 31-Dec-1989 #sequence revision C;Accession: A31345; S04683; S04537  R;Ryder, K.; Nathans, D.  Proc. Natl. Acad. Sci. U.S.A. 85, 8464. A;Title: Induction of protooncogene ce-	A, Reference number: A31345; MUD:89042: A, Accession: A31345 A, Molecule type: mRNA A, Residues: 1-334 <ryd> A, Cross-references: UNIPROT:P05627; UNIR Liamph, W.W.; 639-631, 1988 A, Title: Induction of proto-oncogene JA, Reference number: S04683; MUD:88302-</ryd>	A,Accession: S04683 A,Modecule type: mRNA A,Residues: 1-334 <-LAM> A,Cross-references: UNIPARC:UPI0000001: R,Ryseck, R.P.; Hirai, S.I.; Yaniv, M. Nature 334, 535-537, 1988 A,Title: Transcriptional activation of A,Reference number: S04537; MUID:88302/ A,Accession: S04537 A,Molecule type: mRNA	
EMBO J. 9, 2273-2277, 1990 A;Title: Alternative splicing dictates translational start in Epstein-Barr virus transcr A;Reference number: S12549; MUID:90291993; PMID:2162768 A;Accession: S12549 A;Accession: Compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-135 <rog> A;Cross-references: UNIPROT:Q05614; UNIPARC:UPI000017A7DD</rog>	Alignment Scores:  Pred. No.:  Score:  Score:  B5.00  Matches:  Percent Similarity:  Mismatches:  Mismatches:  A1  Mismatches:  Mismatches:  A2  Gaps:  Gaps:	OS-10-659-782B-11_COPY_112_462 (1-351) x S12549 (1-135)  QY	MetcysGlnThrProTrpProLeuArgProSerGlyProProGlyProArgProGlnGl CCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAGCAGCAGC 	248 TTTCTGGAAGGACGTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGCAGAG 307                  111	Az8896 protein M14 precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 05-Oct-2004 C;Accession: A28996 K;Ann, D. K.; Smith, K.; Carlson, D.M. J. Biol. Chem. 263, 10887-10893, 1988 A;Title: Molecular evolution of the mouse proline-rich protein multigene family. Inserti A;Reference number: A28996; MUID:88273214; PMID:2839509	A; Molecule type: DNA A; Molecule type: DNIPROT: Q62103; UNIPARC: UD100000E6FBE; GB: M23236; GB: J03891; NID: g2: Genetics: 22/1 C; Genetics: 22/1 C; Genetics: 22/1 C; Superfamily: Proline-rich peptide P-B C; Keywords: saliva F; 1-15/Domain: signal sequence #status predicted <ngt> F; 1-15/Domain: signal sequence #status predicted <ngt> Alignment Scores: 2.62 Length: 317 Pred. No.:</ngt></ngt>

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gene BCRF2 protein - human herpesvirus 4
N;Alternate names: gene BMRF1 protein
C;Species: human herpesvirus 4, Esptein-Barr virus
C;Species: human herpesvirus 4, Esptein-Barr virus
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: S32975; S02383; S32976; S32977; S32978; S32979; S32980; S32981; S32982; S32
R;Farrell, P.U.
submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
A;Accession: S32975
A;Accession: S32975
A;Residues: 1-383 <FAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q04397; UNIPROT:QBAZKB; UNIPROT:QBAZKE; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; UNIPROT:QBAZKS; PILA; PID:g1334839; PILA;NOTES: each of the twelve author-supplied translations in EMBL:V01555 for this repeated R;Walls, D; Gannon, F.
EMBO J: 7, 1191-1196, 1988
A;Title: The expression of novel antigens from the Epstein-Barr virus large internal reparterence number: S02381; MUID:88296424; PMID:2841116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: BCRF2_1; BWRF1_2; BWRF1_3; BWRF1_4; BWRF1_5; BWRF1_6; BWRF1_7; BWRF1_9; BWRF1_9, Abote: twelve consecutive ORFs apparently encode the identical polypeptide C;Superfamily: Proline-rich peptide Percent C;Superfamily: Proline-rich peptide antigen C;Keywords: membrane protein; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||
| ProGlyLeuGlnSerProGlyCysProProGluGlyThrLeuGlyValProSerProPro 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||
| ArgSerProLeuSerProValLysProLysGluCysLeuArgGlyAlaThrLeuGlyAla 140
221 GlnHisProArgLeuGlnAlaLeuLysGluGluProGlnThrValProGluMetProGly 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GlnAlaProGluSerArgGlyGlnGlyHisLeuArgValProProArgValProGlyGln 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProGluGlyProArgGlnProGlyArg-----ProGlnArgProValProArgProPhe 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 CACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------ArgAspProSerGlyProAspPro 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTGAACACCAGAGACCTCCACACCTCCCCACAAAGCCCCACATGTTGTTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGGCTTCAGTCTTCTCCCAGAGCACAAAAGACTC-----TGGGTCTGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProThrGlyProSerLeuCysProProAlaProLeuGlnPro 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383
36
7
55
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCATGGCAGGCTCCAGCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x S32975 (1-383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: $02383
A;Molecule type: DNA
A;Residues: 88-144 <WAL>
A;Cross_references: UNIPARC:UPI00002C546; EMBL:X07816
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGCCACTTAGCAACCAGCTCTGTGACCT-----
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Indels:
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Liangeription factor AP-1 - rat

Liangeription factor AP-1 - rat

NiAternate names: transforming protein (jun)

Cispecies: Ratus norvegicus (Norway rat)

Cispecies: Ratus norvegicus (Sachalin, G.; Moveyama, K.)

Nucleic Acids Res, 18, 3400, 1990

A; Ritcheayvashi, 1.; Saka, F.; Gachalin, G.; Yokoyama, K.

Nucleic Acids Res, 18, 3400, 1990

A; Reference number: S12742; MUID:90287724; PMID:211375

A; Residues: 1-34 «KIT-

A; Residues: 1-34 «KIT-

A; Reference number: S20028; MUID:92155155; PMID:1310930

A; Returs: transcriptional regulation of the c-jun gene by retinoic acid and EIA during di
A; Reference number: S20028; MUID:92155155; PMID:1310930

A; Returs: translation not shown

A; Rolecule type: DNA

A; Residues: 1-34 «KIT-

A; Rolecule type: DNA

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                                                                                                                                    ----CCTGAGCCCTGAACA---CCAGAGAGTCCAGGT
                                                                                                      ----GCTGGACTT
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                                                   US-10-659-782B-11_COPY_112_462 (1-351)
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A; Cross-references: UNIPARC: UPI000017C16E; EMBL: X15334
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A Molecule type: mRNA
A Residues: 1-506 <MAR>
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                                                                             C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accession: E72594
C.Accession: E72594
A.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Yamazaki, 
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Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Nov-1994
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LeuSerTrpTrpIleGlnArgProThrThrProAlaProArgThrSerSerThrThrCys
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31 PheIleAlaLeuLysAlaSerSerValSerIleProAsnLeuTrpAlaIleValPhe
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                                                                     hypothetical protein APE1222 - Aeropyrum pernix (strain K1)
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C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Date: 1995 #sequence_revision 19-Oct-1995 #text_change 15-Mar-2004
C;Accession: B56201
R;Martin, J.F.; Miano, J.M.; Hustad, C.M.; Copeland, N.G.; Jenkins, N.A.; Olson, E.N.
R;Martin, J.F.; Miano, J.M.; Hustad, and Copeland, N.G.; Jenkins, N.A.; Olson, E.N.
A)Cl. Cell. Biol. 14, 1647-1656, 1994
A;Title: A Mef2 generates a muscle-specific isoform via alternative mRNA spli
A;Reference number: A56201; MUID:94158837; PMID:8114702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UP10000170C81; GB:S68895; NID:g545521; PIDN:AAB29974.1; PID
C;Genetics:
                                                                                                                                                                                                                                                                                                                                              90 TGAACACCAGAGAGTCCAGGTGAGACCTCCCCACAAAGCCCCACATGTTGTTCCAGCCCT 149
                                                                                                                                                                                                                                                                                                                                                                                                231
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                                                                                                                                                                                       US-10-659-782B-11_COPY_112_462 (1-351) x S16506 (1-381)
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80.50
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RESULT 14
(984865
hypothetical protein At2g43410 [imported] - Arabidopsis thaliana
(c)Species: Arabidopsis thaliana (mouse-ear cress)
(c)Species: Arabidopsis thaliana (mouse-ear cress)
(c)Accession: G84865
(F)Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y.;
(F)Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y.;
(E) W.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Axture 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Genetics:
                                                                                                                                                                                                                                                                                                        A;Residues: 1-744 <SEE>
A;Cross-references: UNIPROT:069995; UNIPARC:UPI0000DAC12; EMBL:AL022374; PIDN:CAA18516.
A;Experimental source: strain A3(2)
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-1056 <STO>
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A; Map position: 2
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Qy         72         CTCCAGCTTCCTGAGCCCTGAACACCA	Qy 120CACAAAGCCCCACATGTTGTTCCAGC 146	147 CCTGCCACTTAGCAACCTGTGACCTGGAGCAGCGCCATCTCTGGGCTTCAGT	Db 794 LeuThrProGlu-Leu 798  Qy 267 GCTTAGAGTCCTAACAGACTGTTTCCCCTTCCAGCAGAAAGGAGTCGAAGAAGCCA 326  Qy 167 CTTAGAGTCCTAAACAGACTGTTTCCCCTTCCAGCAGAAAAGGAGTCGAAGAAAGCCA 326  Qy 267 GCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGCAGAAAAGGAGTCGAAGAAAGCCA 326  Db 799 -LeuAlaThrLeuAlaSerIleLeuProAlaThrSerGlnProAlaAlaProGluSerHi 818	Qy         327 CCAGCCAAGCTGCAGCCC         345           Db         818 sGlnProMetSerGlyPro         824	RESULT 15 B35096 MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported] - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004 C; Accession: B35098 R; Baneriji, J.; Sands, J.; Strominger, J.L.; Spies, T. Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990 A; Title: A gene pair from the human major histocompatibility complex encodes large projections and A; Accession: B35098 A; Accession: B35098 A; Status: preliminary	A,Molecule type: mRNA * ARA> * A.Residues: 1-2142 <ba> * A.Residues: 1-2142 <ba> * A.Residues: 1-2142 <ba> * A.Residues: 1-2142 <ba> * A.Cross-references: UNIPROT: P48634; UNIPARC: UPI000012679F; GB: M33509; NID: g179338; PIDN A;Note: the authors translated the codon AGT for residue 97 as Gly C;Superfamily: collagen alpha 1(IV) chain</ba></ba></ba></ba>	Alignment Scores: 7.32 Length: 2142 Pred. No.: 79.50 Matches: 33 Score: 77.34 Conservative: 11 Best Local Similarity: 28.04 Mismatches: 37 Query Match: 12.34 Indels: 5 B8:	US-10-659-782B-11_COPY_112_462 (1-351) x B35098 (1-2142)	Qy 3 GCCTCCCCAGGACCGTCTGCAGCCTCCTGCTCCGGCATGCTCTGGCTGG	Oy 63 CATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCCCA 122	OY 123 CAAAGCCCCACATGTTGCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGA 179	OY 180 GCAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAC 230

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Distributed under the Creative Commons Attribution-NoDerivs License
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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EMBL, AY184207, AA027351.1; -; mRNA.

EMBL, AY184207, AA027351.1; -; mRNA.

R GN; GO:0005576; C:extracellular region; IEA.

R GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.

R GO; GO:0016791; P:regulation of physiological process; IEA.

R GO; GO:0050791; P:regulation of physiological process; IEA.

R GO; GO:0050791; P:regulation of physiological process; IEA.

BR HTM TEAPRO, IPR006738; motilin ghrelin.

DR PATHR14122; P:reproghrelin; 1.

DR Pfam; PF04644; Motilin ghrelin; 1.

DR Pfam; PF04644; Motilin ghrelin; 1.

DR PRINTS; PR01624; GHRELIN.

SEOUENCE 91 AA; 9972 MW; E7E532D32A3F8609 CRC64;
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Jeffery P.L., Herington A.C., Chopin L.K.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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Matches:
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01-JUN-2003, sequence version 1.
07-FBB-2006, entry version 10.
Exon 3-deleted preproghrelin variant.
                                                                                    06SLF9-9CETA
06SLF2-0DDHE
06SLF4-0DDHE
06SLF4-9CETA
06TGF0-PIG
06SLG3-SHEEP
06SPC3-ANTAM
04SLG3-ANTAM
04SLG3-
Q210G0_PIG
Q6SLG1_CAPHI
Q6SLF6_CEREL
Q4SRQ5_BOSIN
GHRL_BOVIN
Q6SLF9_9CETA
Q6SLF9_9CETA
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-Q=/abss/ABSSMEB spool/US10659782/runat_11072006_110908_2005/app_query.fasta_1
-Q=/abss/ABSSMEB spool/US10659782/runat_11072006_110908_2005/app_query.fasta_1
-DB-Uniprot -QFWT=fastan -SUPFIX=n2p.rup
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OGALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OGTFFFT=pcc -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXEN==200000000 -HOST=abss02p
-USER=US10659782_@CGN 1_1 612_@runat_11072006_110908_2005 -NCPU=6 -ICPU=3
-NO WMAP -NGR SOGRES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33.
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TISSUE-Stomach;
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MEDLINE-20067959; PubMed=10604470; DOI=10.1038/45230;
Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangai
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCGAGCT
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US-10-659-782B-11_COPY_112_462 (1-351) x Q86YP8_HUMAN (1-91)
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MEDLINE=20389976; PubMed=10930375;
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jozdan H., Moore T., Max S. I., Wang J., Hsieh F.,
Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Juschn T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boosk S.A., McZwan P.J., McKernan R.J., Malke J.A.A., Gunzarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brown M. M., Schein J.E., Jones S.J.M., Marra M.A.,
Scherzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=Ghrelin;
IsoId=Q9UBU3-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=Q9UBU3-2; Sequence=VSP_01345;
TISSUE SPECIFICITY: Highest level in stomach. All forms are found
in serum as well. Other tissues compensate for the loss of ghrelin
                                                     MEDLINE=22887296; PubMed=1295309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Clen J., Chowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J.S., Grimandid C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lison D., Mark M.R., Robbie E., Sanchez C., Schoenfield J., Sandren S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Mood W.I., Goddwski P.J., Gray A.M.; The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVIEW.
MEDLINE=21203998; PubMed=11306336; DOI=10,1016/S1043-2760(00)00362-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in growth regulation.

FUNCTION: Obestatin is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal motility (By similarity).

SUBCELIULAR LOCATION: Secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Blood;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Signal peptide prediction based on analysis of experimentally verified cleavage sites."; Protein Sci. 13:2819-2824(2004).
                                                                                                                                                                                                                                                                                                                                                                [6]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
J. Biol. Chem. 278:64-70(2003).
[5]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 24-38.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                            Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                      bioinformatics assessment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
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GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAAGGACTCTGGGTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pubmed=14736731; DOI=10.1210/en.2003-1103; Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J., Suomi S., Hansen B.C.; Characterization of the rhesus monkey ghrelin gene and factors influencing ghrelin gene expression and fasting plasma levels."; Endocrinology 145:2197-2205(2004).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buacchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AGCAGAGAAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGGAGCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-659-782B-11_COPY_112_462 (1-351) x GHRL_HUMAN (1-117)
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Matches:
Conservative:
Mismatches:
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05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 7.
         -> M (in Ref.
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EMBL; AY371699; AAQ74381.1; -; mRNA.
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                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                   -I- MASS SPECTROMETRY: MW=3398.9; MW ERR=0.3; METHOD=Electrospray;
RANGE=24-51 (Ghrelin-28-Cl0); NOTE=0.6 decanoylated form (Ref 4).

I- MASS SPECTROMETRY: MW=3397.2; MW ERR=0.5; METHOD=Electrospray;
RANGE=24-51 (Ghrelin-28-Cl011); MOTE=0-decanoylated form (Ref 4).

I- MASS SPECTROMETRY: MW=3371.3; MW ERR=0.1; METHOD=Electrospray;
RANGE=24-51 (Ghrelin-28); NOTE=0-octanoylated form (Ref 4).

I- MASS SPECTROMETRY: MW=3243.6; MW ERR=0.4; METHOD=Electrospray;
RANGE=24-50 (Ghrelin-27-Cl0); NOTE=0-decanoylated form (Ref 4).

I- MASS SPECTROMETRY: MW=3214.6; MW ERR=0.6; METHOD=Electrospray;
RANGE=24-50 (Ghrelin-27); NOTE=0-octanoylated form (Ref 4).

I- MASS SPECTROMETRY: MW=3114.6; MW ERR=0.6; METHOD=Electrospray;
RANGE=24-50 (Ghrelin-27); NOTE=0-octanoylated form (Ref 4).

I- MASS SPECTROMETRY: MS=3214.6; MW ERR=0.6; METHOD=Electrospray;
MWM="Mtdp://www.infobiogen.fr/services/chromecancer/Genes/GhrelinID327.html".

MWM="Mtdp://www.infobiogen.fr/services/chromecancer/Genes/GhrelinID327.html".

MAMB=RABASE: NAME=Protein Spotlight; NOTE=1ssue 66 of January 2006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R GO; GO:0005615; C:extracellular space; ISS.
R GO; GO:0005645; C:extracellular space; ISS.
R GO; GO:001669; F:g-protein-coupled receptor binding; ISS.
R GO; GO:001669; F:g-protein coupled receptor protein signalin.
R GO; GO:0007186; P:G-protein coupled receptor protein signalin.
R GO; GO:0050791; P:regulation of physiological process; ISS.
R InterPro; IRR006737; motilin_assoc.
R InterPro; IRR006737; motilin_assoc.
R InterPro; IRR006737; motilin_assoc.
R InterPro; IRR006738; motilin_assoc.
R PANTHER; PTHA14122; Preproghrelin; 1.
R PANTHER; PTHA14122; Preproghrelin; 1.
R PERM; PTHA14122; Preproghrelin; 1.
R PRINTS; PRO1624; GRRELIN.
R PRINTS; PRO1624; GRRELIN.
R PRODOM; P0312162; Preproghrelin; 1.
R ProDom; P0312162; Preproghrelin; 1.
R ProDom; P1312162; Preproghrelin; 1.
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Removed in mature form.
/FTIG=PRO 0000019204.
Obestatin (By similarity).
/FTIG=PRO 0000045140.
Removed in mature form (By similarity).
/FTIG=PRO 0000045141.
/FTIG=PRO 0000045141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
synthesis in the stomach following gastrectomy.

The O-n-cotanoylation is essential for ghrelin activity. The O-n-decanoylated forms Ghrelin-27-C10 and Ghrelin-28-C10 differ in the length of the carbon backbone of the carboxylic acid bound to Ser-S. A small fraction of ghrelin, ghrelin-28-C10:1, may be modified with an unsaturated carboxylic acid.

PTM: Amidation of Leu-98 is essential for obestatin activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O-decanoyl serine (in form ghrelin-27-C10 and form ghrelin-28-C10). O-octanoyl serine (in form ghrelin-27 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WWW="http://www.expasy.org/spotlight/back_issues/sptlt066.shtml"
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Missing (in isoform 2),
/FTId=VSP_003245.
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/FTId=PRO 0000019202.
Ghrelin-27.
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EMBL, AJ222278; CAB65733.1; -; mRNA.

EMBL, AR296558; AAG10300.1; -; Genomic_DNA.

EMBL, AS035700; BAB19045.1; -; mRNA.

EMBL, AS359053; AAQ89412.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A59316; A59316; PDB; LP7X; Model; A=1-117.
BDB; LP7X; Model; A=1-117.
Ensembl; ENSG0000157017; Homo sapiens.
H-InvDB; HIX0003050; -
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Contract Topics

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Section & market

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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTTGGACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC
                                              hormone activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 InGinArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity
GO; GO:0050791; P:regulation of physiological process; IEA
InterPro; IPR005738; motilin_assoc.
InterPro; IPR005738; motilin_ghrelin.
PARTHER; PTHR122; Preproghrelin; 1.
Pfam; PF04644; Motilin_assoc; 1.
Pfam; PF04644; Motilin_assoc; 1.
PRINTS; PR01624; GHRELIN; 1.
PRODOM; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg--Ala--
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                                                                                                                                                                                                                                                                                                                                                            117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
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Indels:
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Ensembl; ENSG00000157017; Homo sapiens.
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07-FEB-2006, entry version 7.
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202.00
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43.2%
31.4%
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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Best Local Similarity:
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Q5Y392;
                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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DB:
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Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;

"CDNA cloning of feline and caprine ghrelin.";

submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

"LE WINCTION: Ghrelin is a specific ligand for the growth hormone control of the properties of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).

"It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal motility (By similarity).

"HERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- PTM: Amidation of Leu-98 is essential for obestatin activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
Felinae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) [Contains: Ghrelin; Obestatin].
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
InterPro; IPR005441; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
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Isold=Q6BEG6-2; Sequence=VSP_011626;
-!- PTM: O-n-octanoylation is essential for ghrelin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG 106
21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-659-782B-11_COPY_112_462 (1-351) x Q5Y392_HUMAN (1-36)
                                                                                                                                                      36 AA; 3887 MW; BEAF2F6ABD6968BF CRC64;
                                                                                                                                                                                                                                                 000039
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GABGG; OGBBGS;

25.BEP-2004, integrated into UniProtKB/Swiss-Prot.

13.5EP-2004, sequence version 1.

07-FEB-2006, entry version 17.
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                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
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IsoId=Q6BEG6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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187.00
100.0%
100.0%
29.0%
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Best Local Similarity:
Query Match:
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NCBI_TaxID=9685;
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Pred. No.:
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SEQUENCE
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No
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GHRL FELCA

GHRL FELCA

DT 27-8EB

DT 13-8EB

DT 07-FEB

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**表示部位的** 

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181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AlaMetAlaGlySerPheLeuSerProGluHisGlnLys--Thr------
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                          NUCLEOTIDE SEQUENCE.
PubMed=14724148; DOI=10.1136/gut.2003.021568;
Suzuki H., Masaoka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
                                                                                   Kangawa K., Ishii H., "Helicobacter pylori infection modifies gastric and plasma ghrelin dynamics in Mongolian gerbils.";
                                                                                                                                                                                                                                                                        EMBL; AF442491; AAO06965.1; -; mRNA.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.

GO; GO:0050791; P:regulation of physiological process; IEA.

InterPro; IPR006737; motilin_assoc.

InterPro; IPR006738; motilin_aprelin.

InterPro; IPR00541; Preproghrelin.

PANTHER; PTHR14122; Preproghrelin; 1.

PANTHER; PG4643; Motilin_aprecin; 1.

Pfam; PF04644; Motilin_aprecin; 1.

PFNNTS; PR01624; GHRELIN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-659-782B-11_COPY_112_462 (1-351) x Q8CH53_MERUN (1-117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 1.
27657687FC026A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2004, integrated into UniProtKB/Swiss-Prot. 13-SEP-2004, sequence version 1. 07-FEB-2006, entry version 16.
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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ProDom; PD332162; Preproghrelin,
SEOUENCE 117 AA; 13035 MW; 2
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172.00
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Best Local Similarity:
Query Match:
DB:
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GHRL_CAPHI
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                                                                                                                                                                                                                                                                                                                     /FTIG=PRO 000019201.
Obestatin (By similarity).
/FTIG=PRO 000045138.
Removed in mature form (By similarity).
/FTIG=PRO 0000045139.
Leucine amide (G-99 provides amide group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLysValGln--Gln-----
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Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Gerbillinae; Meriones.
                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR005441; Preproghrelin.
PAWTHER; PFW4643; Motilin_associ.
IPfam; PF04644; Motilin_associ.
IPfam; PF046444; Motilin_aphelin; 1.
PR1NTS; PR01624; GHRELIN.
PROMPS; PR01624; GHRELIN; 1.
Alternative splicing; Amidation; Hormone; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-octanoyl serine (By similarity)
                                                                                                                                                                                                                                                                                                       Removed in mature form (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-659-782B-11_COPY_112_462 (1-351) x GHRL_FELCA (1-117)
                                                                                                                                                                                                                                    By similarity.
Ghrelin (By similarity).
/FTId=PRO_000019200.
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P_011626.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity)
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186.00
41.5%
39.8%
28.9%
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Best Local Similarity:
Query Match:
DB:
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VARSPLIC
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Ghrelin (By similarity).

/FIId=FRO_000019198.

Removed in mature form (By similarity).

/FIId=PRO_000019199.

Obestatin (By similarity).

/FIId=PRO_000045136.

Removed in mature form (By similarity).

/FIId=PRO_000045137.

/FIId=PRO_000045137.
                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                       Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;

"cDNA cloning of felime and caprine ghrelin.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Ghrelin is a specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).

-!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 LysLysProSerGlyArgLeuLysProArgAlaLeuGluGlyGlnPheAspProAspVal
                                                                                                                                                                                                                                                                                                                      sımılarity).
-!- PTM: Amidation of Leu-97 is essential for obestatin activity (By
                                                                                                                                                                                                                                                  intake, and reduces gastric emptying activites and jejunal motility (By similarity).
SUBSCELLUIAR LOCATION: Secreted protein.
PTM: O-n-octanoylation is essential for ghrelin activity (By similarity).
Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-octanoyl serine (By similarity). CDA67971D72E3303 CRC64;
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006737; motilin assoc.
InterPro; IPR006737; motilin assoc.
InterPro; IPR006741; Preproghtelin.
PANTHER; PTHR4122; Preproghtelin.
Pfam; PP04643; Motilin assoc; 1.
Pfam; PP04644; Motilin_ahrelin; 1.
PRIMTS; PR01644; GHRELIN.
ProDom; PD332162; Preproghtelin; 1.
Amidation; Hormone; Lipoprotein; Signal.
SIGNAL
SIGNAL
23 Ghrelin (By s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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                Pecora; Bovidae; Caprinae; Capra
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171.50
56.1%
42.9%
26.6%
                                                             NUCLEOTIDE SEQUENCE [MRNA]
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                               similarity).
                            NCBI_TaxID=9925;
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                                                                             TISSUE=Stomach
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Pred. No.:
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181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
   -CTCTGGGCTTCAGTCTTCTCC 213
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                                   61 GlySerGinGluGluGlyAlaGluAspGluLeuGluIleArgPheAsnAlaProPheAsn
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon 4-deleted mouse
                                                                                                                      214 CAGAGCACAAAGGACTCTGGGTCTGACCTCACTGTTTCTGGAAGGACATGGGGG 267
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Uubhed=15471962; DOI=10.1210/en.2003-1466;

Jeffery F.L., Duncan R.P., Yeh A.H., Jaskolski R.A., Hammond D.S.,

Herington A.C., Chopin L.K.;

Herington A.C., Chopin axis in the mouse: an exon 4-deleted mon proghrelin variant encodes a novel C terminal peptide.";

Endocrinology 146:432-440(2005).
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Ensembl; ENGMUSG000064177; Mus musculus.
MGI; MGI:1930008; Ghrl.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0016608; F:growth hormone releasing hormone activity; RCA.
InterPro; IPR06541; Preproghrelin.
InterPro; IPR06541; Preproghrelin.
PANTHER; PTRA1122; Preproghrelin.
PANTHER; PTRA1122; Preproghrelin; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
                                                                                                                                                      US-10-659-782B-11_COPY_112_462 (1-351) x Q811T4_MOUSE (1-86)
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Mismatches:
Indels:
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Matches:
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Name=Ghrl;
                                                                                                                                                                                                                                                                                                       PRT;
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Q811T4;
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40.7%
178 GAGCAGCAGCGCCAT--
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Best Local Similarity:
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**经**减少1000年中,新州城市,在1980年的城市

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Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., A. Garninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., A. Bajic V.B., Branchas S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidnins V., Allen J.E.,

Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Ambasi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Ambasi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
A. Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
A. Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
A. Crowe M.L., Dalla E., Dalrymple B.P., Regiolini M., Faulkner G.,
A. H. Bernardo D., Down T., Engetrom P., Fagiolini M., Faulkner G.,
A. Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
A. Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
A. Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
A. Kitano H., Maliliam S., Makinan S.P., Kruger A., Kummerfeld S.K.,
A. Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
A. Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
A. Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
A. Rost B., Ruan Y., Salaza S., Reed J., Reid J.F., Ringwald M.,
A. Rost B., Ruan Y., Salazas S., Reed J., Reid J.F., Ringwald C.,
A. Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
                          241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                     Q9EQXO; Q9WUZ1;
113-DEC-2001, integrated into UniProtKB/Swiss-Prot.
01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 39.
Appetite-regulating hormone precursor (Growth hormone secretagogue)
(Growth hormone-releasing peptide) (Motilin-related peptide) (M46
protein) (Contains: Ghrelin; Obestatin).
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000)
                                                                                   301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT
                                                                                                   Kojima M.;
"Mouse mRNA for preproghrelin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
STRAIN=C57BL/6J; TISSUE=Stomach;
PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                 24-30, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY TISSUE-Stomach; MEDLINE=20389976; PubMed=10930375;
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As Sperings Y., Stupkas B., Sugiara K., Sultana R., Takenaha Y., Taki, Tamonja K., Tan. S.L., Tang S., Taylor M.S., Sultana R., Stathada H., Shanada H., Sultana B., Sugiara K., Sultana R., Takenaha Y., Taki, Tamonja K., Tan. S.L., Tang S., Taylor M.S., Tamonja K., Tan. S.L., Tang S., Taylor M.S., Tamonja K., Takenaha Y., Takenayor S., Sultana R., Mido C.L., Mido W., Mido C.L., Mido W., Mido C.L., Mido W., Mido C.L., Matter C., Sasaki D., Tomon. Y. Managaman H., Wallanda M., Managaman M., Managaman M., Managaman M., Makano K., Midolaya M., Managaman M., M
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and introduced the

Name=GHRL; Synonyms=MTLRP;

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GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACTCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Removed in mature form (By similarity).
/FTId=PRO_000019206.
Obestatin (By similarity).
/FTId=PRO_000045142.
Removed in mature form (By similarity).
/FTId=PRO_0000045143.
Leucine amide (G-99 provides amide group)
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        InterPro; IPR006438; motilin_ghrelin.
InterPro; IPR006441; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
Pfam; PF04643; Motilin_ghrelin; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
Promor; PF032162; Preproghrelin; 1.
Alternative splicing; Amidation; Direct protein sequencing; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) [Contains: Ghrelin; Obestatin].
                                                                                                                                                                                                                                                     O-decanoyl serine (in form n-decanoyl ghrelin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-659-782B-11_COPY_112_462 (1-351) x GHRL_MOUSE (1-117)
                                                                                                                                                                                                                                                                                                                            EACB49D2E3CA7203 CRC64
                                                                                                                                                                                                                                                                                                       (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHRL CANFA STANDARD; PRT; 11/ AAA. 13/9BEF8; Q9BEF7; 11/ AAA. 13-DEC-2001, integrated into UniProtKB/Swiss-Prot. 01-JUN-2001, sequence version 1. 07-FEB-2006, entry version 29.
                                                                                                                                             0000019205
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Mismatches:
Indels:
                                                                                                                                                                                                                                            (By similarity)
                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                Ghrelin.
/FTId=PRO_(
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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                                                                                                                                                                                                                                                                                           ghrelin)
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InterPro; IPR006737; motilin_assoc
                                                                                                                                                                                                                                                                                                                               13207 MW;
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40.78
37.38
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                                                                                                        Lipoprotein; Signal SIGNAL 1
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Query Match:
DB:
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Ghrelin (By similarity).
/FTId=PRO_000019196.
/FTId=PRO_000019197.
/FTId=PRO_000019197.
Obestatin (By similarity).
/FTId=PRO_0000045134.
/FTId=PRO_0000045135.
/FTId=PRO_0000045135.
/FUIG=PRO_0000045135.
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                                                                                                                                                                                                                                                                                                                                                                                                      Isold=Q9BBF8-2; Sequence=VSP_003244;
-!- PTM: O-n-octanoylation is essential for ghrelin activity (By similarity).
-!- PTM: Amidation of Leu-98 is essential for obestatin activity (By similarity).
-!- SIMILARITY: Belongs to the motilin family.
           Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                         TISSUE=Gastric fundus;
Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
"Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O-octanoyl serine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD332162; Preproghrelin; 1.
Alternative splicing; Amidation; Hormone; Lipoprotein; Signal.
SIGNAL
PEPTIDE 24 51 Ghrelin (By similarity).
                                                                                                                                      Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3E57FED9D1847CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ298295; CAC29155.1; -; mRNA.
EMBL; AJ298296; CAC29156.1; -; mRNA.
EMBL; AB060700; BAC75929.1; -; mRNA.
Ensembl; ENSCAFG0000005129; Canis familiaris.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006737; motilin_ghealin.
InterPro; IPR006737; motilin_ghealin.
                                                                              NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity)
                                                                                                                                                                                                                                                                                                                                                                     Name=1, Synonyms=Ghrelin,
IsoId=Q9BEF8-1, Sequence=Displayed,
Name=2, Synonyms=del-Gln14-ghrelin,
                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANTHER, PTHR14122; Preproghrelin; 1. Pfan, PPO4643; Motilin, assoc; 1. Pfan; PPO4644; Motilin, ghrelin; 1. PRINTS; PRO1624; GHEELIN
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37
                                                        NCBI_TaxID=9615;
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Hsueh A.J.

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GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appetite-regulating hormone precursor (Growth hormone secretagogue) (Growth hormone-releasing peptide) (Motilin-related peptide) [Contains: Ghrelin; Obestatin-23; Obestatin-13].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 76-95, FUNCTION OF OBESTATIN, CHARACTERIZATION, MASS SPECTROMETRY, AND INTERACTION WITH GPR39.
PubMed=16284174; DOI=10.1126/science.1117255,
Zhang J.V., Ren P.G., Avsian-Kretchmer O., Luo C.W., Rauch R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kangawa K.;
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WACLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), PROTEIN SEQUENCE OF 24-51, MACS SPECTROMETRY, AN ACYLATION OF SER-26.

STRAIN=Sprague-Dawley, TISSUE=Stomach;

MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;

MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;

Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;

"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26. STRAIN-SDARGUE-Dawley; TISGELE-Stomach; MEDLINE=20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
                                                                                                                                                                                                                                                                                                                                          AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Purification and characterization of rat des-Gln14-ghrelin, a
endogenous ligand for the growth hormone secretagogue receptor.
J. Biol. Chem. 275:21995-22000(2000)
                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                      AlametAlaGlySerSerPheLeuSerProGluHisGln--Lys--
                                                                                        (1-117)
                                 166
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Jabec-2001, integrated into UniProtKB/Swiss-Prot.
01-MAY-2000, sequence version 1.
07-MAR-2006, entry version 39.
                              Conservative:
Mismatches:
                                                                                      X GHRL CANFA
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          Length:
Matches:
                                                      Indels:
                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                   US-10-659-782B-11_COPY_112_462 (1-351)
  1.7e-07
168.00
39.8%
37.3%
26.1%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:656-660(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
Alignment Scores:
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IsoId=Q9QYH7-1; Sequence=Displayed;
Name=2: Synonyms=del-Gln14-ghrelin;
IsoId=Q9QYH7-2; Sequence=VSP 003248;
IsoId=Q9QYH7-2; Sequence=VSP 003248;
TISSUE SPECIFICTY: Ghrelin is broadly expressed with higher expression in the stomach. Very low levels are detected in the hypothalamus, heart, lung, pancreas, interestine and adipose tissue. Obestatin is most highly expressed in jejunum, and also found in duodenum, stomach, pituitary, ileum, liver, hypothalamus and heart. Expressed in low levels in pancreas, cerebellum, cerebrum, heart. Expressed in low levels in pancreas, cerebellum, cerebrum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION! Ghrelin is a specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation.
-!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activites and jejunal
                                                                                                                                                                                                                                                                                                                                                               Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
      encoded by the ghrelin gene, opposes ghrelin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the motilin family.
-!- DATABASE: NAME-Protein Spotlight, NOTE-Issue 66 of January 2006;
WWW-"http://www.expasy.org/spotlight/back_issues/sptlt066.shtml"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553; Mateumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y., Tanaka S., Mateun H., Kojima M., Hayashi Y., Kangawa K.; Rangawa R.; Rangawa K.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Amidation of Leu-98 is essential for obestatin activity. MASS SPECTROMETRY: MW=3314.9; MW ERR=0.7; METHOD=Electrospray; RANGE=24-51 (Q9QYH7-1); NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replacement of Ser-26 by aromatic tryptophan preserves ghrelin
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                                                                                                                                                                                                                                                                                                      PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
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PTM: O-n-octanoylation is essential for ghrelin activity.
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GO:0001664; F:G-protein-coupled receptor binding; IPI.
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"Ghrelin: discovery of the natural endogenous ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in gastrointestinal tissue.";
Biochem. Biophys. Res. Commun. 279:909-913(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biophys. Res. Commun. 287:142-146(2001)
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SUBCELLULAR LOCATION: Secreted protein.
ALTERNATIVE PRODUCTS:
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"Obestatin, a peptide enc
effects on food intake.";
Science 310:996-999(2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ghrelin peptides."
                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=21092536;
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withing we will have with

Name=Ghrl; Synonyms=Ghrelin;

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121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
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GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
GO; GO:0007181; P:egulation of physiological process; NAS.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006738; motilin_assoc.
PANTHER; PTHR14122; Preproghrelin.
PANTHER; PTR14122; Preproghrelin, 1.
Pfam; PF04644; Motilin_assoc; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
Prodom; PD332162; Preproghrelin; 1.
Alternative splicing; Amidation; Direct protein sequencing; Hormone;
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Leucine amide (G-99 provides
                                                                                                                                                                                                                                                                                                                            O-octanoyl serine.
Missing (in isoform 2).
/FTId=VSP_003248.
; 8857546FE51A7691 CRC64;
                                                                                                                                                                                                 Removed in mature form.
/FIId=PRO 0000019210.
Obestatin-23.
/FIId=PRO 0000045146.
Obestatin-13 (Probable).
/FIId=PRO 0000045147.
Removed in mature form.
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                                                                                                                                                                                        'FTId=PRO 0000019209.
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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01-JUN-2003, sequence version 1.
07-FBB-2006, entry version 12.
07-FBB-2006, entry version 12.
Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Laurasiatheria, Cetartlodactyla, Ruminantia,
                                                                                                                                                                                           EMBL, AB111891, BAC77409.1; -; mRNA.
Ensembl; RNSMUSG000064177; Mus musculus.
MGI: MGI:1930008 Ghrl.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; RCA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; RCA.
InterPro; IPR006737; mcilin_assoc.
InterPro; IPR005441; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
Pfam; PF046443; Mcilin_assoc; 1.
PRINTS; PR01624; GHRELIN.
                                                                                               NUCLEOTIDE SEQUENCE.
Hisatomi H., Nagao K., Hirata H., Kawano K., Hibi N.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                        ProDom; PD332162; Preproghrelin; 1.
SEQUENCE 78 AA; 8615 MW; AD87CB53C9A22FFB CRC64;
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Mismatches:
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------LysGluAlaProAlaAsp 77
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                                                      Muroidea; Muridae; Murinae; Mus.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                      78 AA;
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Best Local Similarity:
                                                                  NCBI_TaxID=10090;
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Pecora; Bovidae; Bovinae; Bubalus.
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                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AA;
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Best Local Similarity:
                         NCBI_TaxID=89462;
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Q67BBS;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTC---TGTGACCTG 177
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                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 CAGAGCACAAAGGACTCTGGGTCTGACCTCTTTTCTGGAAGGACATGGGGG 267
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13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
Ghrelin precursor (Fragment).
Bubalus bubalis (Domestic water buffalo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria; Laurasiatheria, Cetartiodactyla, Ruminantia;
                                                                                                                                                                                                                                                                                                EMBL; AB060699; BAC75928.1; -; mRNA.

EMBL; DQ294307; ABC00742.1; -; mRNA.

EMBL; DQ294307; ABC00742.1; -; mRNA.

GO; GO:005576; C:extracellular region; IEA.

GO; GO:005791; P:regulation of physiological process; IEA.

InterPro; IPR006739; motilin assoc.

InterPro; IPR006739; motilin_ghrelin.

PANTHER: PTHR1412; Preproghrelin,

PANTHER: PTHR1412; Preproghrelin;

PEm; PF04644; Motilin_ghrelin;

PEm; PF04644; Motilin_ghrelin;

PEm; PF04644; Motilin_ghrelin;

PEM; PF04644; Motilin_ghrelin;

PRNINTS; PR01624; GHRELIN.
                  Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.; "sheep ghrelin.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               Lv D.Y., Cao G.F., Bai C.L., Xu R.G.;
"Mongolia sheep ghrelin mRNA.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 Potential.
50 ghrelin.
12977 MW; B78ECA3DBF0E568E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-659-782B-11_COPY_112_462 (1-351) x Q863L0_SHEEP
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Matches:
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157.50
55.18
40.8%
24.5%
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116 AA;
                                                                                                          NUCLEOTIDE SEQUENCE
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Best Local Similarity:
TISSUE=Stomach;
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Q45RQ6;
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21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLysLeuGlnArgLygGluPro 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Baviskar P.S., Mitra A., "Characterization of ghrelin gene of zebu cattle (Bos indicus) and buffaloes (Bubalus bubalis)."; Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     EMBL, DQ118139, AAZ38152.1; -; Genomic_DNA.
GO, GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
GO; GO:0050791; P:regulation of physiological process; IEA.
InterPro; IPR005441; Preproghrelin.
Pfan; PF04644; Motilin ghrelin; 1.
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-659-782B-11_COPY_112_462 (1-351) x Q45RQ6_BUBBU (1-49)
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Mismatches:
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11-0CT-2004, sequence version 1.
07-FEB-2006, entry version 6.
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GO, GO:0050791; P:regulation of physiological process; IEA. InterPro; IPR006738; motilin ghrelin. InterPro; IPR005738; motilin ghrelin. PANTHER; PTHR1412; Preproghrelin; 1. Pfam; PF04644; Motilin ghrelin; 1. Pfam; PR04644; GRREIN. 1. NOW TER. SEQÜENCE 74 AA; 7980 MW; 875424C2D41FC166 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 2 Sequence 3

26538, A 25834, A

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30696, A 19224, A

Sequence 3 Sequence 3 Sequence 1

311, App 29947,

17391, A 31903, A 21426, A

Sequence 3 Sequence 2 Sequence 1 Sequence 3

2453, Ap 1330, Ap

Sequence Sequence Sequence

10, A. 11505, A. Appl

Sequence 1 Sequence 1

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Sequence:

Title: Perfect

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US-09-989-735-268

US-09-989-726-268

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US-09-989-728-268

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US-09-989-728-268

US-09-989-293A-268

US-09-252-991A-26834

US-09-252-991A-26538

US-09-252-991A-17391

US-09-980-016-11505

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US-10-276-392-1

US-10-276-392-1

US-10-276-392-1

US-10-276-392-1
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COUNTY: SEADABLE FORM: DESCRIPTION TYPE: DISKRETE COMPUTER: IBM Compactible OPERATING SYSTEM: DOS SOFTWARE: FastESE (For Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09046479
Patent No. 6291653
GENERAL INFORMATION:
APPLICANT: Sheppard, Faul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: ZymoGenetics, Inc.
1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Savislar, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
  CLASSIFICATION:
                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: Se
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-MODEL=frame+ n2p.mcdel -DEV=xlp
-MODEL=frame+ n2p.mcdel -DEV=xlp
-Q=/abss/ABS/RBS spool/US10659782/runat_11072006_110915_2118/app_query.fasta_1
-Q=/abss/ABS/RBS spool/US10659782/runat_11072006_110915_2118/app_query.fasta_1
-DB=1ssued_Patenfes_AA -QFWT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MINS_0 -ALIK MINS_0 -ALIKH ADDE=15
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abss02p -USER=US10659782_@CGN_1 1_78 @runat_11072006_110915_2118 -NCFU=6
-ICPU=3 -NOW MAPP -NBC_SCORES=0 -WAIT -DSPREACK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Sequence 268, App
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1280.135 Million cell updates/sec
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Sequence 2, Apr
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Sequence 28, Apr
Sequence 268, A
Sequence 268, A
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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                              - protein search, using frame_plus_n2p model
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US-08-82-89-70-2
US-09-608-81.0A-4
US-09-404-411A-2
US-09-94-987-2
US-09-991-181-268
US-09-990-444-268
US-09-990-444-268
US-09-997-333-268
US-09-997-333-268
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                                                                                                                                     US-10-659-782B-11_COPY_112_462
644
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPOTER: IBM COMPOTER: LEM COMPO
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08822897C Patent No. 6380158
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 117 amino acids TYPE: amino acid sTRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
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204.00
44.18
43.28
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity:
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Pred. No.:
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61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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Conservative:
Mismatches:
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APPLICANT: Sheppard, Stephen R.
APPLICANT: Delsher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR PILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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ATTORNEY/AGENT INFORMATION:
NAME: Sawislar, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPHONE: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                4.98e-15
204.00
44.1%
43.2%
31.7%
                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 117 amino acids
                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
   61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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                                                                                                                                                                                                                                                                       301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
                                                                                                                                                                                                                                                                                         COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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Matches:
Conservative:
Mismatches:
Indels:
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STREEF: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/046,479
FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:

NAME: Sawislak, Deborah A

REFERENCE/DOCKET NUMBER: 37,438

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sheppard, Paul O.
Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANIEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID 1
US-09-794-987-2
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09794987; Patent No. 6838438; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity:
Query Match:
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Mismatches:
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Matches:
Conservative:
Mismatches:
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Patent No. 6627729
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: TML PEPTIDES
FILE REFERENCE: 97-04C1
CURRENT FAPLICATION NOMBER: US/09/404,417A
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 117
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-404-417A-2
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DB: 2 Gaps: 1	ò	181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
US-10-659-782B-11_COPY_112_462 (1-351) x US-09-794-987-2 (1-117)	qq	37 37
Oy 1 ATGCCCTCCCGAGGACCGTCTGCAGCCTCCTCGGCATGCTCTGGCTGG	λ <sub>0</sub>	241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAAACAGACTGTTTCCCCCTTCC 300
Db 1 MetProSerProGlyThrValCysSerLeuLeuGlyWetLeuGlyMetLeuAspLeu 20	qq	37 37
Qy         6.1 GCCATGGCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCC 120	oy Op	301 AGCAGAGAAAGGAGTCGAAGAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
121 CACAAGCCCACATGTTGCAGCCTTAGCAAGCAAGCTAAGGAAGG	RESIII.T	
37	US-09-9	US-09-91-181-268 , Sequence 268, Application US/09991181
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240	; Paten	Patent No. 6913919 GENERAL INFORMATION:
Db 37 37	; APPL ; APPL	
Oy 241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300	APPL ; APPL	APPLICANT: Betstein, David APPLICANT: Desnoyers, Luc
Db 37 37	APPL APPL	<b></b> .
Qy 301 AGCAGAGAAAGAGTCGAAGAAGCCACCAGCCAGCTGCAGCCCCGAGCT 350	APPL	
Db 38ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52	; APPL	
RESULT 6 US-09-863-253-2	, APPI	
; Sequence 2, Application US/09853253 ; Patent No. 6897286	, APPL	APPLICANT: Kljavin, Ivar J. APPLICANT: Napier, Mary A.
; GENERAL INFORMATION: ASPERS. STEPHEN	, APPL	
; APPLICANT: SHEPPARD, PAUL . ADDI-ICANT: DETSHER THERES.	APPL	Roy, Margaret A
; APPLICANT: BISHOP, PAUL	APPL	ICANT: Tunes, Daniel
; TITLE OF INVENTION: ZS1g33-like Peptides ; FILE REFERENCE: 00-30	, APPL	ICANT: Watanabe, Colin K. ICANT: Williams, P. Mickey
; CURRENT APPLICATION NUMBER: US/09/853,253 ; CURRENT FILING DATE: 2001-05-10	, APPI ; APPI	
; PRIOR APPLICATION NUMBER: 60/203,300 ; PRIOR FILING DATE: 2000-05-11	TILL ;	; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ; TITLE OF INVENTION: Acids Encoding the Same
; NUMBER OF SEQ ID NOS: 28 ; SOFTWARE: FastSEQ for Windows Version 3.0	; FILE	REFERENCE: P2730P1C53 ENT APPLICATION NUMBER: US/09/991,181
; SEQ ID NO 2 ; LENGTH: 117	CURR	ENT FILING DATE: 2001-11-16 R APPLICATION NUMBER: 60/049787
TYPE: PRT : ORGANISM: Homo sabiens	, PRIC	R FILING DATE: 1997-06-16 R APPLICATION NUMBER: 60/062250
US-09-853-253-2	; PRIC	R FILING DATE: 1997-10-17 R APPLICATION NIMBER: 60/065186
1	PRIC	FILING DATE: 1997-11-12
4.98e-15 Lengin: 204.00 Matches:	, PRIC	A REFLICATION NOWBERS: 00/003311 R FILING DATE: 1997-11-16
larity: 44.1% Conservative: imilarity: 43.2% Mismatches:	, PRIC	R AFFLICATION NUMBER: 60/066//0 R FILING DATE: 1997-11-24
Query Match:       31.7*       Indels:       66         DB:       2       Gaps:       1	, PRIC	R APPLICATION NUMBER: 60/075945 R FILING DATE: 1998-02-25
00-11 CODY 112 A62 (1-261) \$ 110-00-863-963	, PRIC	R APPLICATION NUMBER: 60/078910 R FILING DATE: 1998-03-20
	PRIC	R APPLICATION NUMBER: 60/083322
1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTGGGATGCTCTGGGCTAGCTTG	PRIC	R FILING DATE: 1998-04-28 R APPLICATION NUMBER: 60/084600
l MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuIrpLeuAspLeu	, PRIOR , PRIOR	R FILING DAIE: 1998-05-0/
Oy 6.1 GCCATGGCAGGTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACTCCCCC 120	PRIOR	K FILING DAIE: 1998-U5-26 R APPLICATION NUMBER: 60/08/607 R FILING DAIE: 1998-06-02
121 CACAAAGCCCCACATGTTCCAGCCCTGCCACTTAGCAACCTCTGTGACCTGGAG	PRIC ; PRIC	R APPLICATION NUMBER: 60/087609 R FILING DATE: 1998-06-02
2.7	PRIOR	R APPLICATION NUMBER: 60/087759 R FILING DATE: 1998-06-02
	, PRIC	R APPLICATION NUMBER: 60/087827

06-03 : 60/088021 : 60/088025 06-04 : 60/088026 : 60/088028 : 60/088028 : 60/088028 : 60/088029 : 60/088030 : 60/088030	0.6 0/088326 0.6 0/088326 0.6 0/088167 0.6 0/088212 0.6 0/088212 0.6 0/088212 0.6 0/088213 0.6 0/088213 0.6 0/088213 0.6 0/088213 0.6 0/088742 0.6 0/088742 0.6 0/08838 0.6 0/08824 0.6 0/088826 0.6 0/088826	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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APPLICATION PILING DATES	
1.	Pred. No Score: Percent

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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/076945
PRIOR APPLICATION NUMBER: 60/076910
PRIOR APPLICATION NUMBER: 60/08302
PRIOR PILING DATE: 1998-03-29
PRIOR PILING DATE: 1998-03-29
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
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PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-07
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 
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                                                                                                                                                  1 ATGCCCTCCCCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTTG 60
                                                                                                                                                                                                                                                                       APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
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                                                                                                   US-10-659-782B-11_COPY_112_462 (1-351) x US-09-991-181-268 (1-117)
    Mismatches:
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/06511
PRIOR APPLICATION NUMBER: 61/06511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J. Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Kljavin, Ivar J. Napier, Mary A. Pan, James Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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Best Local Similarity:
Query Match:
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PRIOR PELICATION WOMBER: 60/08958

PRIOR PELICATION WOMBER: 60/089589

PRIOR PELICATION WOMBER: 60/089599

PRIOR PELICATION WOMBER: 60/089600

PRIOR PELICATION WOMBER: 60/089601

PRIOR PELICATION WOMBER: 60/089901

PRIOR PELICATION WOMBER: 60/080901

PRIOR PELICATION WOMBER: 60/080901

PRIOR PELICATION WOMBER: 60/080901

PRIOR PELICATION WOMBER: 60/08001

PRIOR PELICATION WOMBER: 60/08001
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	PRIOR FILING DATE: 1998-07-01   PRIOR PAPELICATION NUMBER: 60/091519   PRIOR PAPELICATION NUMBER: 60/091626   PRIOR PAPLICATION NUMBER: 60/091626   PRIOR DATE: 1998-07-02   PRIOR PAPLICATION NUMBER: 60/091633   PRIOR PILING DATE: 1998-07-02   PRIOR FILING DATE: 1998-07-07   PRIOR FILING DATE: 1998-07-07   PRIOR PILING DATE: 1998-07-07   PRIOR APPLICATION NUMBER: 60/091982   PRIOR PILING DATE: 1998-07-07   PRIOR PAPLICATION NUMBER: 60/09182   PRIOR PILING DATE: 1998-07-07	
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	US-10-659-782B-11_COPY_112_462 (1-351) x US-09-990-444-268 (1-117)	
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	Qy       61 GCCATGGCAGGCTCCAGCTTCCTGAACCCCGAAACACCAGAGAGTCCAGGTGAGACCTCCC	37
	Qy 121 CACAAAGCCCCCACATGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG	18
<u>.</u>	Db 37	37
	Qy 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC	24
	Db 37	37
	Qy 241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCTTCC	30
-	Db 37	37
	Qy 301 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAGCTGCAGCT 350 	
	RESULT 9 US-09-796-158-2 ; Sequence 2, Application US/09796158 ; Sequence 2, Application US/09796158 ; Patent No. 693590 ; GENERAL INFORMATION:	

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Gurney, Austin L.
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APPLICANT:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/046,479
FILING DATE: «Unknown»
ATORNEY/AGENT INFORMATION:
NAME: Sawislad, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELEPHONE: 206-442-6678
TELEFAX: «OF 42-6678
                                                                                                                                                                                                                                                                                                             LENGTH: 117 amino acids
TYPE: amino acid
STYPE: amino acid
STYANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi J.
APPLICANT: Baker. Kevin P.
APPLICANT: Botstein, David
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Grimaldi, J. Christopher
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Raton, Dan L.
Ferrara, Napoleone
Pong, Sherman
Gerber, Hanspeter
Gerritsen, Manspeter
Goddard, Audrey E.
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US-09-997-333-268
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Pred. No.:
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APPLICANT: WILLIAM: W
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Williams, P. Mickey
Wood, William I.
                                                                                                                    Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                       Paoni, Nicholas F.
Kljavin, Ivar J.
Napier, Mary A.
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PRIOR PRINCATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-66-10
PRIOR FILING DATE: 1998-66-10
PRIOR FILING DATE: 1998-66-10
PRIOR FILING DATE: 1998-66-10
PRIOR PELLING DATE: 1998-66-10
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PRIOR PELLING DATE: 1998-66-17
PRIOR PELLING DATE: 1998-66-19
PRIOR PELLING DATE: 1998-66-22
PRIOR PELLING DATE: 1998-66-22
PRIOR APPLICATION NUMBER: 60/09043
PRIOR PELLING DATE: 1998-66-22
PRIOR APPLICATION NUMBER: 60/09043
PRIOR PELLING DATE: 1998-66-24
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	PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090542 DBTOD FILING DATE: 1908-06-24
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PR	IOR FILING DATE: 1998-06-25
PR	PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/09696
PR	IOR FILING DATE: 1998-06-25
PR	ION FILLIAMING AND 1998-06-26
P. Y.	IOR FILING DATE: 1998-06-26
, PR	IOR APPLICATION NUMBER: 60/091360 IOR FILING DATE: 1998-07-01
PR	IOR APPLICATION NUMBER: 60/091478 TOR PILING DATE: 1998-07-02
PR	IOR APPLICATION NUMBER: 60/091544
	IOR FILING DATE: 1998-07-01 IOR APPLICATION NUMBER: 60/091519
PR	IOR FILING DATE: 1998-07-02 IOR APPLICATION NUMBER: 60/091626
PR	FILING DATE: 1998-07-02
, , , PR.	IOR AFFLICATION NUMBER: 60/091633 IOR FILING DATE: 1998-07-02
PR	
PR	APPLICATION NUMBE
, PR	ှ ငွ
, PR.	FILING DATE: 1998-07-09
Alignment Pred. No.:	Scores: 4.98e-15 Length:
Score:	204.00 Matches:
Percel Best	Percent Similarity: 44.1% Conservative: 1 Best Local Similarity: 43.2% Mismatches: 0
Query DB:	1.7% Indels: Gaps:
US-10	-659-782B-11_COPY_112_462 (1-351) x US-09-997-333-268 (1-117)
6	1 AIGCCTCCCCAGGGACCGTCTGCAGCCTCCTCGCCTGGCTCTGGCTGG
d d	1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
δλ	61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
đ	21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln 37
ò	121 CACAAAGCCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
셤	37 37
ò	181 CAGCAGCGCCATCTCGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
a a	37 37
ď	241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
qq	37 37
ò	301 AGCAGAGAAAGGGTCGAAGAAGCCCCCAGCCAAGCTGCAGCCCCGAGCT 350
qa	38ArglysGluSerLysLysProProAlaLysLeuGlnProArgAla 52

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
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CURRENT PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 1997-66-16
PRIOR PELING DATE: 1997-66-16
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066710
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/08910
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-03
PRIOR PELICATION NUMBER: 60/08802E
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08802E
                                                                     Sequence 268, Application US/0992598
Patent No. 6556108
GENERAL INFORMATION:
APPLICANT: Bakerazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostetain, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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Gerritsen, Mary E.
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RESULT 11
US-09-992-598-268
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PRIOR APPLICATION NUMBER: 60/088030
PRIOR PLINED DATE: 1938-0-6-04
PRIOR PLINED DATE: 1938-0-6-05
PRIOR PLINED DATE: 1938-0-6-10
PRIOR PLINED DATE: 1938-0-6-17
PRIOR PPLICATION NUMBER: 60/08950
PRIOR PLINED DATE: 1938-0-6-17
PRIOR PLINED DATE: 1938
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181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
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                                                                                    121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln---61n------ 37
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FITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR PELICATION NUMBER: 60/06250
PRIOR PELICATION NUMBER: 60/062250
PRIOR PELICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/083322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 268, Application US/09989735; Patent No. 6972185; GENERAL INFORMATION:
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Goddard, Audrey
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Botstein, David
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US-09-989-735-268
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Conservative:
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Indels:
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                                                                     PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1938-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR PELING DATE: 1938-06-24
PRIOR PELING DATE: 1938-06-24
PRIOR PELING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR PELING DATE: 1938-06-25
PRIOR PELING DATE: 1938-07-01
PRIOR PELING DATE: 1938-07-01
PRIOR PELING DATE: 1938-07-02
PRIOR PELING DATE: 1938-07-07
PRIOR PELING DATE: 1938-
                                                R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
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Best Local Similarity:
Query Match:
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Pred. No.:
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NUMBER: 60/087607 1998-06-02 1998-06-02 1998-06-02 NUMBER: 60/08759 1998-06-02 NUMBER: 60/087827 NUMBER: 60/088021 1998-06-04 NUMBER: 60/088025 1998-06-04 NUMBER: 60/088025	88-06, 88-06, 88-88-88-88-88-88-88-88-88-88-88-88-88-	NUMBER: 60/08858 1998-06-11 1998-06-11 1998-06-11 NUMBER: 60/088876 1998-06-11 NUMBER: 60/089105 1998-06-16 NUMBER: 60/089440 1998-06-16 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089514 1998-06-16 NUMBER: 60/089514 1998-06-17 NUMBER: 60/089518 1998-06-17 NUMBER: 60/08959
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RELING DATE: 1997-10-17

RAPPLICATION NUMBER: 60/065186

RAPPLICATION NUMBER: 60/065311

RELING DATE: 1997-11-12

RELING DATE: 1997-11-13

RELING DATE: 1997-11-24

RAPPLICATION NUMBER: 60/078945

RAPPLICATION NUMBER: 60/078910

RELING DATE: 1998-02-25

RAPPLICATION NUMBER: 60/08910

RELING DATE: 1998-04-28

RELING DATE: 1998-06-02

RAPPLICATION NUMBER: 60/084600

RELING DATE: 1998-06-02

RAPPLICATION NUMBER: 60/08759

RELING DATE: 1998-06-02

RAPPLICATION NUMBER: 60/08700

RAPPLICATION NUMBER: 60/08700

RELING DATE: 1998-06-02

RELING DATE: 1998-06-03

RELING DATE: 1998-06-03

RELING DATE: 1998-06-03

RELING DATE: 1998-06-03

RELING DATE: 1998-06-04

RAPPLICATION NUMBER: 60/088028

RELING DATE: 1998-06-04

RELING DATE: 1998-06-06-04

RELING DATE: 1998-06-06-06

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R APPLICATION NUMBER: 60/088742
R APPLICATION NUMBER: 60/088742
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R APPLICATION NUMBER: 60/08810
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088810
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08824
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
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APPLICATION UNDBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088861
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  PRIOR 
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR PILING DATE: 1997-06-16
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Matches:
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Mismatches:
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Patent No. 7018811
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Pan,James
Paoni,Nicholas F.
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## APPLICATION NUMBER: 60/090863  # FILING DATE: 1998-06-26  # FILING DATE: 1998-06-26  # APPLICATION NUMBER: 60/091360  # APPLICATION NUMBER: 60/091478  # APPLICATION NUMBER: 60/091544  # FILING DATE: 1998-07-01  # APPLICATION NUMBER: 60/091519  # FILING DATE: 1998-07-02  # APPLICATION NUMBER: 60/091636  # APPLICATION NUMBER: 60/091638  # APPLICATION NUMBER: 60/09198  # APPLICATION NUMBER: 60/09182  # APPLICATION NUMBER: 60/09182  # APPLICATION NUMBER: 60/09182	core:	US-10-659-782B-11_COPY_112_462 (1-351) x US-09-989-726-268 (1-117)	1 ATGCCTCCCCAGGGACCGTCTGCAGCCTCCTCGGCATGCTCTGGCTGG	61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120	121 CACAAAGCCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180	37 37	181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240	37 37	241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300	37 37	301 AGCAGAGAAAGGGTCGAAGAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350	514-268 5.268, Application US/09997514 6. 7019116 INFORMATION: NT: Baker, Kevin P. NT: Batterin, David NT: Betterin, David NT: Eaton, David NT: Forgy, Sherman NT: Forgy, Sherman NT: Gerber, Hanspeter NT: Gerdard, Audrey NT: Goddard, Audrey NT: Goddard, Audrey NT: Grimaldi, J. Christopher NT: Grimaldi, J. Christopher
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PRIOR APPLICATION NUMBER: 60/088742
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PRIOR APPLICATION NUMBER: 60/089105
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TITLE OF INVENTION: Secreted and Transmembrane FILLE OF INVENTION: Secreted and Transmembrane FILLE OF INVENTION: Secreted and Transmembrane FILLE OF INVENTION: Acids Encoding the Same FILLE OF INVENTION INVERS: 60/665186

PRIOR APPLICATION NUMBER: 60/665111

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PRIOR PILLING DATE: 1998-06-05

PRIOR PILLING DATE: 1998-06-06

PRIOR PILLING DATE:
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Williams, P. Mickey
Wood, William I.
                                                                                                                     Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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         Kljavin, Ivar J
                                    Napier, Mary A.
Pan, James
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APPLICATION NUMBER: 60/090542

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DR FILING DATE: 1998-06-25
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DR APPLICATION NUMBER: 60/090690
DR APPLICATION NUMBER: 60/090694
DR FILING DATE: 1998-06-25
DR APPLICATION NUMBER: 60/090696
DR FILING DATE: 1998-06-25
DR APPLICATION NUMBER: 60/090862
DR FILING DATE: 1998-06-26
DR APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
                   APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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APPLICANT: Wood, William II.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE REFERENCATION NUMBER: US/09/989,728
CURRENT PELLING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-11-17
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PRIOR PELLING DATE: 1998-06-03
PRIOR PELLING DATE: 1998-06-04
Sequence 268, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Gerritsen, Mary E
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Kljavin, Ivar J.
                                                                                                       APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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PRIOR APPLICATION NUMBER: 60/090355

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DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/08828

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DR APPLICATION NUMBER: 60/08828

R FILING DATE: 1998-06-11
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	PRIOR		1998-06-24			
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Sequence:

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NG-10-659-782A-32
Sequence 32, Application US/10659782A
Publication No. US20050059015A1
Sequence 32, Application Wo. US20050059015A1
Septence 32, Application No. US20050059015A1
TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing, TITLE OF INVENTION: Monitoring and Treating Obesity and/or Diabetes
FILE REFERENCE: 28238
CURRENT APPLICATION NUMBER: US/10/659,782A
CURRENT FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 116
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Mismatches:
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Gaps:
US-09-991-073-268
US-09-991-0442-268
US-09-991-0442-268
US-09-991-0442-268
US-09-991-044-268
US-09-992-298-268
US-09-992-298-268
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US-09-991-104-268
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Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 268, App
                                                                       July 11, 2006, 16:51:53; Search time 24.5 Seconds (without alignments) 1990.879 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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            GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-647-191A-3
US-10-477-506-2
US-09-794-987-2
US-09-989-722-268
US-09-989-723-268
US-09-989-723-268
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Maximum Match 100%
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext
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                                         Sequence 2, Application US/10477506;
Publication No. US20040157227A1
General Informations
Hubblication No. US20040157227A1
General Informations
APPLICANT: Chopin, Lisa K
APPLICANT: Jeffery, Penelope L
APPLICANT: Herington, Adrian C
TILLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
FILE REFERENCE: 225:81
CURRENT FILING DATE: 2003-11-10
FRIOR PRILOR TILING DATE: 2001-12-17
PRIOR PLICATION NUMBER: PR4919
PRIOR FILING DATE: 2001-15-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3:1
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Matches:
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Sequence 2, Application US/09794987
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
Deláber, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
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US-09-794-987-2
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Sequence 3, Application US/10294191A
Sequence 3, Application US/10294191A
Sequence 3, Application No. US20030211512A1
Sequence 3, Application No. US20030211512A1
Sequence 3, Application No. US2003021151A1
Septicant: Kim, Kwam Suk
APPLICANT: Kim, Kwam Suk
APPLICANT: Anderson, Lloyd L.
TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing
FILE REPERENCE: POS40831
CURRENT APPLICATION NUMBER: US/10/294,191A
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 16
SOFTHANG PAPLICATION NUMBER: US 60/333,222
SOFTHANG PAPLICATION NUMBER: US 60/333,222
SEQ ID NOS: 16
LENGTH: 60
                                                                                                     CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
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21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro
                                                    41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu
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ORGANISM: Human
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Pred. No.:
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APPLICANT: SHEPPARD, PAUL
APPLICANT: BISHOP, PAUL
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zsig33-like Peptides
FILE REPRENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASESEQ for Windows Version 3.0
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Gerritsen, Mary E
                     STEPHEN
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Botstein, David
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Eaton, Dan L.
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US-09-853-253-2
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Query Match:
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   GENERAL INFORMATION:
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LENGTH: 117
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66
                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                 FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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204.00
44.1%
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31.7%
CITY: Seattle
STATE: WA
COUNTRY: USA
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Query Match:
DB:
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Pred. No.:
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61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
                                                                                                                                                                                                                                                                                                                                         121 CACAAAGCCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                       181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
                                                                                                                                                                                                     241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
                                                                                                                                                                                                                                                                                    21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln-----
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  117
51
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66
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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APPLICANT:
APPLICANT:
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RETLING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088888
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08916
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-12
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R FILING DATE: 1998-06-24
R PILING DATE: 1998-06-24
R PILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090445
R APPLICATION NUMBER: 60/09045
R APPLICATION NUMBER: 60/090472
R APPLICATION NUMBER: 60/090472
R APPLICATION NUMBER: 60/090472
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090540
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090542
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/089512
R APPLICATION NUMBER: 60/089514
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
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R APPLICATION NUMBER: 60/08558

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653
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R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
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R RILING DATE: 1998-06-22
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R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
R APPLICATION NUMBER: 60/090429
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
   FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
ALING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089907
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      APPLICANT: Roy, Margaree Am.
APPLICANT: Roy, Margaree Am.
APPLICANT: Story Margaree Am.
APPLICANT: Story Margaree Am.
APPLICANT: STORY Margaree Am.
APPLICANT: Walkenbb. Collin K.
APPLICANT: STARTON Secreted and Transmembrane Polypeptides and Nucleic Tills OF INVESTION's Acids Emcoding the Same
TILLS OF INVESTION'S ACID TO THE SAME SO TO SAME
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REPRENCE: P2730PLG2.

CURRENT FILE OF INVENTION: Acids Encoding the Same POLYPEPTION: Acids Encoding the Same CURRENT FILE OF INVENTION: Acids Encoding the Same CURRENT FILE OF INVENTION: Acids Encoding the Same PRIOR FILING DATE: 2001-111-13

PRIOR PLILOR DATE: 1997-10-17

PRIOR PLILOR DATE: 1997-10-12

PRIOR PLILOR DATE: 1997-11-13

PRIOR PLILOR DATE: 1997-11-13

PRIOR PLILOR DATE: 1997-11-14

PRIOR PLILOR DATE: 1997-11-24

PRIOR PLILOR DATE: 1999-02-25

PRIOR PLILOR DATE: 1999-02-25

PRIOR PLILOR DATE: 1999-02-25

PRIOR PLILOR DATE: 1999-05-26

PRIOR PLILOR DATE: 1999-06-07

PRIOR PLICATION WINDER: 60/08028

PRIOR PLILOR DATE: 1999-06-07

PRIOR PLILOR DATE
Sequence 268, Application US/09989723
Patent No. US20020072092A1
SENERAL INFORMATION:
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                           Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                           Gerber, Hanspeter
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                                                                                                                                       Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kljavin, Ivar J.
                                                                                                       PPLICANT: Ashkenazi, Avi J
                                                                                                                                                                                                                                                                                                                                                                                                               Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Napier, Mary A.
                                                                                                                                                                                                                                                                                                               Fong, Sherman
                                                                                                                                                                                                                                           Eaton, Dan L.
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Matches:
Conservative:
Mismatches:
Indels:
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                     PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR PELING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
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Best Local Similarity:
Query Match:
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Pred. No.:
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PRIOR FILING DATE: 1998-06-04

PRIOR FILING DATE: 1998-06-04

PRIOR FILING DATE: 1998-06-05

PRIOR PLICATION NUMBER: 60/08625

PRIOR FILING DATE: 1998-06-05

PRIOR PLICATION NUMBER: 60/08635

PRIOR FILING DATE: 1998-06-10

PRIOR PLING DATE: 1998-06-10

PRIOR FILING DATE: 1998-06-10

PRIOR PLING DATE: 1998-06-10
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US-10-659-782B-11_COPY_112_462 (1-351) x US-09-989-723-268 (1-117)
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Matches:
Conservative:
Mismatches:
Indels:
                      R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090435
R APPLICATION NUMBER: 60/090445
R APPLICATION NUMBER: 60/090444
R APPLICATION NUMBER: 60/090444
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 6//092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
  60/090429
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APPLICATION NUMBER: 60/090557
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R APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/08910S
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/088217
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   181 CAGCAGCGCCATCTCTGGCCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
                                                                                                                                 241 CTCACTGTTTCTGGAAGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 300
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CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR PELICATION NUMBER: 60/06250

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-24

PRIOR FILING DATE: 1997-11-24

PRIOR PRIOR APPLICATION NUMBER: 60/075945

PRIOR APPLICATION NUMBER: 60/075945

PRIOR APPLICATION NUMBER: 60/075910

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-06-07

PRIOR APPLICATION NUMBER: 60/081302

PRIOR FILING DATE: 1998-06-07

PRIOR APPLICATION NUMBER: 60/08160

PRIOR APPLICATION NUMBER: 60/08160

PRIOR APPLICATION NUMBER: 60/08160

PRIOR PILING DATE: 1998-05-28
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Sequence 268, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/087609
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Grimaldi,J.Christopher
Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Botstein, David
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APPLICANT: Gurney, Austin 1.
APPLICANT: Gurney, Austin 1.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Najer, Mary A.
APPLICANT: Najer, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: 80/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
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                Length:
Matches:
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Batent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Betein, David

APPLICANT: Betein, David

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerber, Hanspeter

APPLICANT: Gedard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Gramaldi, J. Christopher
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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PRIOR FILING DATE: 1996-02-25
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PRIOR FILING DATE: 1996-02-25
PRIOR PELICATION NUMBER: 60/08105
PRIOR FILING DATE: 1996-02-20
PRIOR PELICATION NUMBER: 60/08106
PRIOR FILING DATE: 1996-05-28
PRIOR PELING DATE: 1996-05-28
PRIOR PELING DATE: 1996-06-02
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PLING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/09163
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PRIOR PILING DATE: 1998-07-07
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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
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Gerber, Hanspeter
Gerriteen, Mary E.
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Godowski, Paul J.
Grimaldi, J. Christopher
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Ferrara, Napoleone
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Napier, Mary A.
Pan, James
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Best Local Similarity:
Query Match:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/989,731

CURRENT APPLICATION NUMBER: 06/06226

PRIOR PILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1998-02-25

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PRIOR PILING DATE: 1998-02-26

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PRIOR PILING DATE: 1998-02-28

PRIOR PILING DATE: 1998-02-29

PRIOR PILING DATE: 1998-02-39

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NUMBER: 60/088810 1998-06-10 NUMBER: 60/088824 1998-06-10 NUMBER: 60/088826 1998-06-10 NUMBER: 60/08861 1998-06-11 NUMBER: 60/08876 11998-06-11 NUMBER: 60/08876 11998-06-11 NUMBER: 60/08976	28. 60 (08951) 28. 60 (08951) 28. 60 (08951) 29. 06-16 20. 10 (08953) 28. 60 (08953) 28. 60 (08953) 28. 60 (08959) 28. 60 (08959) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08990) 28. 60 (08995) 28. 60 (08995) 28. 60 (08995) 28. 60 (08995) 28. 60 (08995) 28. 60 (08995) 28. 60 (08995) 28. 60 (08995)	
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RESULT 11 US-09-989-732-268 ; Sequence 268, Application US/09989732

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PRIOR APPLICATION NUMBER: 60/08326
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR PRILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-17
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PRIOR PLILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-12
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APPLICANT: Watanabe, Colin K.
APPLICANT: Shang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT PLICATION WURBER: 05/049797
PRIOR PILING DATE: 1997-06-16
PRIOR PLILING DATE: 1997-11-13
PRIOR PLILING DATE: 1997-11-13
PRIOR PELICATION WURBER: 60/065311
PRIOR PELICATION WURBER: 60/065310
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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  Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkennzi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan L.
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181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 240
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PICIS
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
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Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, David
APPLICANT: Ferrara, Napoleone
APPLICANT: Foog, Sherman
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PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075910
PRIOR PELING DATE: 1998-03-25
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-07-07
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APPLICATION NUMBER: 60/087609
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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LICATION NUMBER: 60/090676
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ING DATE: 1998-06-25
                                                     LICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/091519
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NUMBER: 60/087759 1998-06-02 NUMBER: 60/087827 1998-06-03 NUMBER: 60/088021 1998-06-04 NUMBER: 60/088025 1998-06-04 NUMBER: 60/088028 1998-06-04 NUMBER: 60/088028 1998-06-04 NUMBER: 60/088028 1998-06-04 NUMBER: 60/088028	0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	WEER: 6 998 - 06 - 998
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
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PRIOR PLICATION NUMBER: 60/08052
PRIOR PLICATION NUMBER: 60/090246
PRIOR PLICATION NUMBER: 60/090252
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/09069
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PRIOR PRIDATION NUMBER: 60/09069
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PRIDATION DATE: 1998-00-22
PRIOR APPLICATION NUMBER: 60/090153
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Alignment Scores:

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PRIOR APPLICATION NUMBER: 60/06571
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/07845
PRIOR RILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/07810
PRIOR APPLICATION NUMBER: 60/08102
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-28
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-05-07
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PRIOR PILING DATE: 1998-06-02
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PRIOR PILING DATE: 1998-06-04
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730910CE: P2730910CE: P2780CE: P2790CE: P27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AGCAGAGAGAGGGGGGGAGGCCACCAGCAGCTGCAGCCCCGGAGCT 350
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Patent No. US20020132252A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Gerber, Hanspeter
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Napier,Mary A.
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Botstein, David
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                                                                     Percent Similarity:
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US-09-990-442-268
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A APPLICATION NUMBER: 6/089653
BRILING DATE: 1998-06-17
BRILING DATE: 1998-06-17
BRILING DATE: 1998-06-18
BRILING DATE: 1998-06-19
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R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
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R APPLICATION NUMBER: 60/090444

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R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R RILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-25
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61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 120
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Matches:
Conservative:
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Indels:
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PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1988-07-02
PRIOR PELING DATE: 1988-07-02
PRIOR PELING DATE: 1988-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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PRIOR PILING DATE: 1998-07-07
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Patent No. US20020132253A1
GENERAL INFORMATION:
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Geddard, Audrey
Goddowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Eaton, Dan L.
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Paoni, Nicholas F

APPLICANT:

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R APPLICATION NUMBER: 60/08940

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

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R APPLICATION NUMBER: 60/089514

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R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

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R APPLICATION NUMBER: 60/089598

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R FILING DATE: 1998-06-17
                                                                                                        R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088618
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088876
R APPLICATION NUMBER: 60/08876
R APPLICATION NUMBER: 60/089105
R APPLICATION NUMBER: 60/089105
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
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R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
R PILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
   FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089653
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/089952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090535
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   PRILICAR PRI
                                                                                                                                                            TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C17

CURRENT APPLICATION NUMBER: US/09/991,163

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-11-17

PRIOR PILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13

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R APPLICATION UNMBER: 60/088030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

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APPLICATION UNMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088810
                                                    Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/
FILING DATE: 1998-06-04
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APPLICANT: SOCIAL MILLIAM 1.

APPLICANT: SOCIAL MILLIAM 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION WHERE: 60/06250

PRIOR APPLICATION WHERE: 60/06250

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-11-13

PRIOR PLING DATE: 1997-11-12

PRIOR PRIOR PRIOR OF ENCOMER: 60/06311

PRIOR PRIOR PRIOR OF ENCOMER: 60/06310

PRIOR PRIOR PRIOR DATE: 1998-00-25

PRIOR PRIOR PRIOR DATE: 1998-00-25

PRIOR PRIOR PRIOR OF ENCOMER: 60/08302

PRIOR PRIOR PRIOR DATE: 1998-00-25

PRIOR PRIOR PRIOR DATE: 1998-00-26

PRIOR PRIOR PRIOR DATE: 1998-00-00

PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                Grimaldi, J. Christopher
Gurney, Austin L.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                   Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                              Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
                                        APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                           Kljavin,Ivar J.
Napier,Mary A.
                                                                                                                                 Desnoyers, Luc
                                                                                                                                                                                                               Fong, Sherman
                                                                                                                                                             Eaton, Dan L.
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Matches:
Conservative:
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Indels:
Gaps:
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PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090694
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
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Best Local Similarity:
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US-09-993-604-268 ; Sequence 268, Application US/09993604 ; Patent No. US20020137075A1

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PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089514

PRIOR APPLICATION NUMBER: 60/089514

PRIOR APPLICATION NUMBER: 60/089532

PRIOR PILING DATE: 1998-06-17

PRIOR PILING DATE: 1998-06-17

PRIOR PILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089599

PRIOR APPLICATION NUMBER: 60/089599

PRIOR PILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089600

PRIOR PILING DATE: 1998-06-17

PRIOR PILING DATE: 1998-06-17

PRIOR PILING DATE: 1998-06-17

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PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19
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DR APPLICATION NUMBER: 60/08105

DR FILING DATE: 1998-06-12

DR FILING DATE: 1998-06-16

DR FILING DATE: 1998-06-16

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DR PELING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089512

DR FILING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/08953

DR FILING DATE: 1998-06-17

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DR FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/08953
R APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/088655
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R APPLICATION NUMBER: 60/088734
R APPLICATION NUMBER: 60/088738
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
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R PILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088881
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
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R PAPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
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R APPLICATION NUMBER: 60/090429
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<u>п</u> ,	RIOR	APPLICATION NUMBER:	N NUMBER: 60/09047	72	3		4
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, Di	PRIOR	APPLICATION	N NUMBER: 60/09069	95			
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<u>.</u>	PKIOK	APPLICATION	N NUMBER: 60/090862	29			
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	20179	FILING DATE	: 00/09:	70			
	PRIOR	APPLICATION	NUMBER: 60	82			
<u>а</u>	PRIOR	FILING DATE	E: 1998-07-09				
Aliq	nment	Scores:					
Pred	Pred. No.:		3.19e-11	Length:	117		
Score		:	204.00		51		
Perce	ent s Loca	ent Similarity: Local Similari	44.1% tv: 43.2%	Conservative: Mismatches:	10		
Query	V Mat	Match:	•	Indels:	99		
DB:			· M	Gaps:			
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ò		1 ATGCC	crecceaegeaccerci	GCAGCCTCCTGCTCCTC	GGCATGCTCT	9	0
q		1 MetPr			GlyMetLeuT	2	0
ò		61 GCCAT	GGCAGGCTCCAGCTTCC	TGAGCCTGAACACCAG	SAGAGTCCAGG	TGAGACCTCCC 12	20
gg		21 AlaMe	tAlaGlySerSerPheL	AlametalaglySerSerPheLeuSerProGluHisGlnArgValGln	Argvaldin-	n	7
ò		121 CACAA	AGCCCCACATGTTGTTC	CACAAAGCCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG	PACCAGCTCT		180

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Sequence 6, Application US/11255699
Sequence 6, Application US/11255699
Sequence 6, Application WO. US2006105393A1
GENERAL INFORMATION:
APPLICANT: APFEL. CHRISTIAN
APPLICANT: EODERLE, THILO
APPLICANT: EOFEWANN, SANNAH JENSEN
APPLICANT: PENSKI, MIREILLE
TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS
FILE REFERENCE: 22817
CURRENT APPLICATION NUMBER: US/11/255,699
CURRENT APPLICATION NUMBER: B04105285.3
PRIOR FILING DATE: 2004-10-25
PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 117
FUNDE: PARTIES APPLICATION VERSION 3.3
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US-11-174-3078-1839
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Mismatches:
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Matches:
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44.18
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31.78
 ORGANISM: Homo sapiens
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Query Match:
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US-11-255-699-6
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Sequence 33, Appl
Sequence 40, Appl
Sequence 170, Appl
Sequence 34, Appl
Sequence 34, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Appli
Sequence 3905, Ap
Sequence 31196, A
                                                                                                                 (without alignments)
1009.077 Million cell updates/sec
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                                                                                                    July 11, 2006, 16:52:28 ; Search time 2.8 Seconds
                GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                        protein search, using frame_plus_n2p model
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US-11-299-697-3905
US-10-953-349-31196
US-11-257-498-35
US-11-257-498-40
US-11-257-498-40
US-11-293-329-170
US-11-293-34
US-11-293-697-4118
                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                            US-10-659-782B-11_COPY_112_462
644
                                                                                                                                                                                                                                                                                                         112942 segs, 26832045 residues
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, Ygapext
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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12.9
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score:

Title: Perfect

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Scoring table:

Sequence 2054, Ap Sequence 42, Appl Sequence 49268, A Sequence 11453, A Sequence 534, App

(1-117)

(1-351) x US-11-255-699-6

US-10-659-782B-11\_COPY\_112\_462

93.5 883.5 83.5 80.5

26459789

Result No.

117 51 1 0 66

Sequence 2723, p. 18 Sequence 2723, p. 18 Sequence 21149, A Sequence 21149, A Sequence 2014, Ap Sequence 1816, Ap Sequence 1870, A Sequence 1870, A Sequence 2732, Ap Sequence 1428, Ap Sequence 34296, A Sequence 34295, A Sequence 34296, A Sequence

828, App 2402, Ap 3446, Ap

Sequence Seq

40356, F

Sequence

, Appl

Met ProSer Prodiy Thrval Cysser LeuLeuLeuCalyMet Leu TrpLeu Asplea 20   Db   132   Cyse Prodiy Thrval Cysser LeuLeuLeuCalyMet Leu TrpLeu Asplea 20   Db   132   Cyse Prodiy Thrval Cyse Treated Concade Accordence Canada		US-10-659-782B-11_COPY_112_462 (1-351) x US-10-953-349-31196 (1-297)	CAGCTT         80         201 TTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGG           ::                         ::                         SerIlePheSer         52         aSerThrProArgArgProAlaAlaSerSerAla           CAAAGC         Qy         261 ATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCC           ::                                   ProThrAlaGly         72         Bb         82 r	
1 61 21 121 181 37 241 37 301	RESULT 23.697-3905  'Sequence 3905, Application US/11293697  'Sequence 3905, Application US/11293697  'Publication No. US20060105376A1  'GENERAL INFORMATION:  'TITLE OF INVENTION: NOVEL full length cDNA  'FILE REFERENCE: HI-A0106  'CURRENT APPLICATION NUMBER: US/11/293,697  'CURRENT FILING DATE: 2005-12-05  'RIOR APPLICATION NUMBER: US/10/108,260  'PRIOR FILING DATE: 2002-03-28  'NUMBER OF SEQ ID NOS: 5458  'SOFWARE: Patentin Ver. 2.1	TYPE: PRT   1910   19	27 CCTCCTGCTCTGGCTTGGCTTGGCCATGGCCAGGTCCAGCTT	129 CCCACATGT
	RESULT US-11-2	; TYPE: PR: ; ORGANISM US-11-293-69 Alignment Sc Pred. No.: Score: Score: Percent Simi Best Local Simi Best Local Subs: US-10-659-78	8 6 6 6	666666

Page

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APPLICANT: Bachmann, Martin F
APPLICANT: Bachmann, Martin F
APPLICANT: Bachmann, Martin F
APPLICANT: Saudan, Philippe
TITLE ON Saudan, Philippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FILE REFERENCE: 1700.0540001
CURRENT APPLICATION NUMBER: US/11/257,498
CURRENT APPLICATION NUMBER: 60/621,465
PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
LENGTH: 28
             267 GCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGCAGAAAGGAGTCGAAGAAGCCA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326
                              ----GlnGlnArgLysGluSerLysLysPro 21
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Publication No. US20060134670A1

GENERAL INFORMATION:

APPLICANT: PIU, Fabrice

TITLE OF INVERTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR

TITLE OF INVERTION: HORMONE NUCLEAR RECEPTORS

FILE REFERENCE: ACADIA.043A

CURRENT APPLICATION NUMBER: US/11/283,329

CURRENT FILING DATE: 2005-11-18

PRIOR APPLICATION NUMBER: 60/629,811

FRIOR APPLICATION NUMBER: 60/629,811

NUMBER OF SEQ ID NOS: 242

SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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'Sequence 40, Application US/11257498
'Publication No. US20060088550A1
'GENERAL INFORMATION:
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46.8%
42.6%
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; ORGANISM: Homo sapiens
US-11-283-329-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Felis catus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 -----
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Best Local Similarity:
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APPLICANT: Saudan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FILE REFERENCE: 1700.0540001
CURRENT APPLICATION NUMBER: US/11/257,498
FILOR APPLICATION NUMBER: 05/621,465
PRIOR APPLICATION NUMBER: 05/621,465
PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bachmann, Martin F
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurija, Alma
APPLICANT: Saudan, Phillippe
TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used ther
FILE REFERENCE: 1700.0540001
CURRENT APPLICATION NUMBER: US/11/257,498
CURRENT FILING DATE: 2005-10-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 CTTCTCCCAGAGCACAAAGGACTCTGGGTCTGACCTCACTGTTTCTGGAAGGACATGGGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GlnGlnArgLysGluSerLysLysPro 21
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PRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33
LENGTH: 28
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46.8%
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13.4%
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ORGANISM: homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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Alignment Scores:

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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION WUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34427
LENGTH: 251
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LOCATION: (65). (65)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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Matches:
Conservative:
Mismatches:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HELLX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 4118
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CORGANISM: Homo sapiens
US-11-293-697-4118
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Publication No. US20060088550A1
Sequence 34, Application WS/11257496
Publication No. US20060088550A1
GENERAL INFORMATION.
APPLICANT: Bachmann, Martin F
APPLICANT: Saudan, Phillippe
FILE REFERENCE: 1700.054.0001
CURRENT APPLICATION NUMBER: 00/621,465
FRIOR FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SEQ ID NO 34
LENGTH: 28
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US-11-293-697-4118
; Sequence 4118, Application US/11293697
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Best Local Similarity:
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Pred. No.:
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US-11-257-498-34
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LOCATION:
OTHER INFORMATION: PFam Name:
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SEQ ID NO 1082
LENGTH: 1238
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OTHER INFORMATION: PFam
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LOCATION:
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NAME/KEY: misc_feature
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ORGANISM: Zea mays
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|---AsnGlnThrCysHisProGlyCysHisCysProSerGlyMetLeuLeuLeuValSer 3604
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| So CysGlySerProSerThrSerArgSerThrSerProProProAlaSerSerThrSer 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 TGAGGTCAGACCCAGAGTCCTTTGTGC-----TCTGGGAGAAGACTG-----AAG 200
                                                                                                                                                                                                                                    CTTCCTGAGCCCTGAACACCCAGAGAGTCCAGGTGAGACCTCCCCACAAAGCCCCACATGT 137
                                                                                                                                                                                                                                                                    132 GlnProArgProAspArgProThrSerPro-----AlaSerProArgArgThrSerSer 149
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                 251
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PUblication No. US20060086532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
FRIOR APPLICATION NUMBER: US 60/363,019
FRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
                                               Conservative:
Mismatches:
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US-10-505-928-150
Alignment Scores:
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LENGTH: 5738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: GI Number: 16293; NR Description: glycine rich protein
OTHER INFORMATION: [Arabidopsis thaliana] >gi|72320|pir||KNWU glycine-rich cell
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name: S-antigen; PFam Description: S-antigen protein
                                               3636 GlyTrpGly---ProTrpGlyProTrpSerHisCysSerArgSerCysGlyGlyGlyLeu 3654
199 CCCAGAGATGGCGCTGCTCCAGGTCACAGAGCTGGTTGCTAAGTGGCAGGGCTGGAA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secretin_N; PFam Description: Bacterial type
                                                                                                                                        139 CAACATGTGGGGGTTTGTGGGGAGGTCTCACCTGGACTCTCTGGTGTTCAGGGCTCAGGA 80
                                                                                                                                                                                                                                                                                79 AGCTGGAGCCTGCCATGGCCAAGTCCAGCCAGAGCATGCCGAGGAGGAGGCTGCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1082, Application US/11174307B
Publication No. US20060143729A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USECULE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USECUL FOR MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
                                                                                                                                                                                    Dehydrin; PFam Description: Dehydrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3655 ArgSerArgThrArgAla 3660
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GI Number: 50948247; NR Description: putative pepper esterase [Oryza sativa (japonica cultivar-group)] sgi|42407543|dbj|BAD10748.1| putative pepper esterase [Oryza sati (japonica cultivar-group)] sgi|42408724|dbj|BAD09942.1| putative
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 21593183; NR Description: unknown [Arabidopsis thaliar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esterase (Capsicum
                                                                                                                                                                                      domain
                                                                                                                   Carboxylesterase
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                                                                                                                                                                                      Protein kinase
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                                               Name: Pyr_redox_2; PFam Description: Pyridine
                                                                                                                                                                                                                                                        Homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: GI Number: 48714603; NR Description: putative
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Matches:
Conservative:
Mismatches:
Indels:
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79.50
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NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: PFam
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OTHER INFORMATION: PFam
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OTHER INFORMATION: S
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; OTHER INFORMATION:
US-11-174-307B-936
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Best Local Similarity:
Query Match:
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NAME/KEY:
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                                             PEATURE:
NAME/KEY: misc_feature
LOCATION:
COTHER INFORMATION: GI Number: 34898126; NR Description: putative glycine-rich
OTHER INFORMATION: cell wall protein precursor [Oryza sativa (japonica
OTHER INFORMATION: cultivar-group)] >gi|24059890|dbj|BAC21356.1| putative glycine-ri
OTHER INFORMATION: cell wall protein precursor [Oryza sativa (japonica
                                GI Number: 7636182; NR Description: glycine-rich protein
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NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: PFam Name: Abhydrolase_3; PFam Description: alpha/beta
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Matches:
Conservative:
Mismatches:
Indels:
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; Bublication No. US2006014372941
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TTLE OF INVENTION: UNCLEOTIDE SEQUENCES AND ITLILE OF INVENTION: UNCLEOTIDE SEQUENCES AND ITLILE OF INVENTION: UNCLEOTIDE SEQUENCES AND ITLILE OF INVENTION: UNSFELL FOR MODIFYING PLANFILLS OF INVENTION: UNBER: US/11/174,307B
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
                                                                                                                                                                                                                                                                                                                 Gaps:
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79.50
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26.8$
NAME/KEY: misc_feature
                               INFORMATION:
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Best Local Similarit
Query Match:
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US-11-174-307B-936
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395 AlaLeuArgSerArgGlyLeuGlnProGlySerLeuGlnSerLeuGlnProAlaProArg 414
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474 nThrlleAlaSerThrSerProSerGluArgAlaGlyMetAlaHisSerProSerLeuSe 494
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Conservative:
Mismatches:
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR PRIOR DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PETENTIN Ver. 2.1
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Best Local Similarity:
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US-10-449-902-41125
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LENGTH: 940
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CONA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-06-29
PRIOR PILING DATE: 2003-06-29
PRIOR PELICATION NUMBER: UP 2002-203269
PRIOR PELICATION NUMBER: UP 2002-383870
PRIOR PELICATION NUMBER: US/10/2-383870
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 34826
LENGTH: 312
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MONA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
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Publication No. US20060123505A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
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US-10-449-902-34826
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